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(54) Title: NUCLEIC ACIDS, PROTEINS, AND ANTIBODIES

(57) Abstract: The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

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Nucleic Acids, Proteins, and Antibodies

[1] This application refers to a "Sequence Listing" that is provided only on electronic media in computer readable form pursuant to Administrative Instructions Section 801(a)(i). The Sequence Listing forms a part of this description pursuant to Rule 5.2 and Administrative Instructions Sections 801 to 806, and is hereby incorporated in its entirety.

[2] The Sequence Listing is provided as an electronic file (PTZ13PCT_seqList.txt, 5,421,455 bytes in size, created on January 13, 2001) on four identical compact discs (CD-R), labeled "COPY 1," "COPY 2," "COPY 3," and "CRF." The Sequence Listing complies with Annex C of the Administrative Instructions, and may be viewed, for example, on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, version 2000 (see World Wide Web URL: <http://www.fileviewer.com>).

Field of the Invention

[3] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to

these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

[4] Enzymes comprise a large subset of proteins which function as catalysts for biochemical reactions. In fact, virtually every biochemical reaction involves the catalytic activity of an enzyme or enzymes. Most enzymes are located intracellularly, but there are a number of enzyme families which are either secreted into the extracellular space, or associated with the plasma membrane. Some enzymes, including the secreted digestive enzymes trypsin and pepsin, are produced as inactive precursors called zymogens, which require chemical modification to become active. In many cases, the catalytic activity of an enzyme depends on its association with a cofactor. Cofactors may be organic molecules, termed coenzymes, or metal ions. Many coenzymes are derived from vitamins.

[5] Enzymes contain two important functional units: the substrate binding site, and the catalytic site. The substrate-binding site consists of a cleft which is geometrically complementary to the shape of the preferred substrate. In addition, the amino acid residues which form the substrate binding site have noncovalent interactions with the amino acids of the complementary substrate region. The catalytic site is the portion of the molecule that facilitates the biochemical reaction once the substrate is bound to the enzyme. For a more extensive discussion of enzyme properties, see Biochemistry, Voet and Voet (1990); and Molecular Cell Biology, 2nd Edition, Darnell et al. (1990).

[6] The International Union of Biochemistry and Molecular Biology (IUBMB) has established enzyme nomenclature guidelines to provide an organizational framework to the growing field of enzymology (see Enzyme Nomenclature, Academic Press (1992), or the IUBMB Nomenclature Committee web site at the URL address: <http://www.chem.qmw.ac.uk/iubmb/enzyme>). According to the IUBMB guidelines, all enzymes can be categorized by the chemical reaction they catalyze. Documented enzymes are assigned an identifier which takes the form of "EC [A.B.C.D]", where A is one of the major functional classes of enzymes (1 through 6; see below); B and C designate increasingly specific

subgroups of enzymatic reactions; and D represents the arbitrary number of an individual member of a given category. As an example, the enzyme acetylcholinesterase is designated EC 3.1.1.7, because it is a member of the class of hydrolases (EC 3.-.-.-), acting on ester bonds (EC 3.1.-.-), in the subgroup of carboxylic ester hydrolases (EC 3.1.1.-), and it is assigned number 7. Descriptions of the six major functional classes, including notable examples of each, follow below.

Oxidoreductases (EC 1.-.-.-)

[7] Enzymes of this class catalyze oxidation-reduction reactions. Sub-classification is according to the substrate group oxidized (e.g., CH-OH, CH-CH, and CH-NH₂, to name but a few). A representative member of this enzyme class is long-chain-alcohol dehydrogenase (EC 1.1.1.192), which is involved in lipid metabolism. Deficient activity of this enzyme has been shown to be the primary cause of Sjogren-Larsson syndrome, an autosomal recessive disorder characterized by the presence of ichthyosis, mental retardation, and spasticity (Rizzo *et al.*, *J. Clin. Invest.* 81: 738-744 (1988)).

Transferases (EC 2.-.-.-)

[8] Catalytic reactions of transferases are characterized by the transfer of a chemical group from a "donor" molecule to an "acceptor" molecule. Transferases can be subgrouped according to the chemical group transferred. For example, amino transferases (EC 2.6.-.-) transfer nitrogenous groups, and methyltransferases (EC 2.1.1.-) transfer methyl groups. Often the transferred group is donated by a coenzyme. A major subgroup of transferase enzymes are the protein kinases (EC 2.7.-.-), which catalyze the transfer of a phosphate group from ATP to a substrate protein. Protein kinases, such as calcium/calmodulin dependent (CaM) kinase II (EC 2.7.1.123), are known to play important roles in signal transduction pathways (Kennedy, *Brain Res Brain Res Rev* 26(2-3):243-57 (1998)). Other transferases are involved in metabolic processes. For example, guanidinoacetate N-methyltransferase (GAMT; EC 2.1.1.2), converts guanidinoacetate into creatine, which is essential for the maintenance of energy reserves in the form of ATP. GAMT deficiency causes neurological impairments which may include progressive extrapyramidal movement disorders, seizures, developmental delay, and muscular dystonia (Stockler *et al.*, *Pediat. Res.* 36:409-413 (1994)).

Hydrolases (EC 3.-.-)

[9] Enzymes of this class catalyze the splitting of a substrate into two fragments by the addition of a water molecule; the water's hydroxyl group being incorporated in one fragment and the hydrogen atom in the other. Hydrolases can be subcategorized according to the chemical bond involved. For example, peptidases (EC 3.4.-.-; also known as proteases) are hydrolases which catalyze the breaking of peptide bonds. Pepsin (EC 3.4.23.1), a digestive protease which has been implicated in a number of gastrointestinal disorders, is an example of a proteolytic hydrolase enzyme (see, for example, Hirschowitz, *Yale J. Biol. Med.* 72(2-3):133-43 (1999), and Del Bianco et al., *Dig. Liver Dis.* 32(1):12-9 (2000)). Deficient activity of beta-glucocerebrosidase (EC 3.2.1.45), an O-glycosyl hydrolase, is associated with Gaucher's disease. Symptoms of Gaucher's disease include bone lesions, skin pigmentation, enlargement of the liver and spleen, and, in some cases, neurological impairments.

Lyases (EC 4.-.-)

[10] Lyases cleave C-C, C-O, C-N, and other bonds by means other than hydrolysis or oxidation. The reverse reaction is performed by a synthetase. Histidine decarboxylase (EC 4.1.1.22) is a carboxy-lyase that converts histidine to histamine, a biogenic amine involved in a number of physiologic processes, including inflammation, allergic responses, neurotransmission, and gastric acid secretion. The phosphorus-oxygen lyase, adenylate cyclase (EC 4.6.1.1), is an intracellular enzyme which acts on ATP to form adenosine 3', 5'-cyclic phosphate (cAMP), a second messenger activator of protein kinase activity.

Isomerases (EC 5.-.-)

[11] Members of this class of enzymes catalyze geometric or structural changes within a molecule to form an isomer. Subclasses of isomerases include racemases / epimerases (EC 5.1.-.-), *cis-trans*- isomerases (EC 5.2.-.-), intramolecular isomerases (EC 5.3.-.-), intramolecular transferases (EC 5.4.-.-), and intramolecular lyases (EC 5.5.-.-). Protein disulfide isomerase (PDI; EC 5.3.4.1) catalyzes the intramolecular rearrangement of disulfide bonds, thus contributing to the folding of newly-synthesized proteins at the endoplasmic reticulum (see, for example, Luz and Lennarz, *EXS* 77:97-117 (1996)). Autoantibodies to PDI have been implicated in hepatic disorders (Nagayama et al., *J Toxicol Sci* Aug;19(3):163-9 (1994)).

Ligases (EC 6.--.-)

[12] Ligase enzymes catalyze the formation of a bond between two substrate molecules, coupled with the hydrolysis of a pyrophosphate bond in ATP or a similar triphosphate. A well characterized example of this class is DNA ligase 1 (EC 6.5.1.1), which catalyzes the joining of DNA fragments (via the formation of a phosphodiester bond) during DNA replication, recombination, and repair. Mutations in the gene encoding DNA ligase 1 have been linked to immunodeficiency disorders and hypersensitivity to DNA-damaging agents (Barnes et al., *Cell*, 69, 495-503 (1992)).

[13] The discovery of new human enzyme polynucleotides, the polypeptides encoded by them, and antibodies that immunospecifically bind these polypeptides, satisfies a need in the art by providing new compositions which are useful in the diagnosis, treatment, prevention and/or prognosis of a range of conditions, including but not limited to cancer, immunodeficiencies, neurological disorders, and metabolic disorders.

Summary of the Invention

[14] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

[15] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1A. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The fourth column provides the sequence identifier, "SEQ ID NO:X", for each of the contig sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in

Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification

number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

[16] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

[17] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X"

that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[18] The PFAM identification disclosed in Table 2, columns 5 and 6, communicates both the function and enzymatic activity of polypeptides corresponding to the PFAM. Extensive documentation on PFAM families and individual members of these families are maintained in publicly accessible databases (see, for example the Sanger Centre PFAM web server at <http://www.sanger.ac.uk/> for a searchable PFAM database). Using this information, and included links to PROSITE, SWISSPROT, GenBank, and other sequence databases, one can routinely assign an EC (Enzyme Commission) code to the polypeptides. The EC code consists of 4 integers separated by decimal points that are used to classify enzymes, and indicate important information about cellular function and enzyme mechanism. The first digit indicates a broad group of enzyme mechanism (i.e. 1=oxidoreductases, 2=transferases). The second digit indicates the type of substrate the enzyme acts upon or a broad subcategory of the enzyme type (i.e. EC 1.6 oxidoreductases acting on NADH or NADPH, or 5.1=racemases and epimerases, a subtype of EC 5=isomerases). The third digit is used to distinguish further characteristics (EC 1.1.1 oxidoreductases acting on the CH-OH group of donors with NAD or NADP as the acceptor, versus EC 1.1.2 where a cytochrome acts as the acceptor) or is simply assigned as 1 for the all entries where further clarification is unnecessary (all members of EC 4.1, carbon-carbon lyases are in group 4.1.1). The final number designates a specific enzyme, for instance, EC 4.1.1.1 pyruvate decarboxylase, or EC 1.1.1.1 alcohol dehydrogenase. Thus, if all of the source sequences for the PFAM have EC codes of the form 1.1.3.X, where X is a positive integer, the polypeptide being evaluated is likely to have a similar EC code, and, in this example, will likely be an oxidoreductase acting on the CH-OH group of donors with oxygen as an acceptor.

[19] Furthermore, knowledge of PFAM identification and/or EC code for a polypeptide communicates enzymatic activity of the protein. This activity can routinely be confirmed using or modifying assays known in the art. Additionally, these assays may routinely be applied or modified to evaluate the enzymatic activity of fragments and variants of the invention. Further, these assays may routinely be applied or modified to

evaluate the ability of agonists or antagonists of the invention (e.g., agonistic or antagonistic antibodies) to enhance or reduce this enzymatic activity, respectively.

[20] Table 3 provides polynucleotide sequences that may be disclaimed according to certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

[21] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1A, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used

to generate the library.

[22] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1A, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM, McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 9, as determined using the Morbid Map database.

[23] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

[24] Table 7 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

[25] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

[26] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[27] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

[28] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[29] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID names with SEQ ID NO:X. Thus,

starting with an SEQ ID NO:X, one can use Tables 1, 6 and 7 to determine the corresponding Clone ID, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[30] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[31] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein), and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[32] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished

through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[33] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[34] Of course, a polynucleotide which hybridizes only to polyA⁺ sequences (such as any 3' terminal polyA⁺ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[35] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[36] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[37] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1A or 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded

by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1A.

[38] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

[39] The PFAM accession number disclosed in Table 2, column 6 provides a link, through publicly accessible databases (see, for example the Sanger Centre PFAM web server at <http://www.sanger.ac.uk/>, and included links to PROSITE, SWISSPROT, GenBank, and other sequence databases), to the associated EC code, or closely-related EC codes. As described above, EC codes provide a description of the biochemical reaction(s) catalyzed by an enzyme family. Based on the associated EC code(s), one can routinely test the polypeptides of the invention for functional activity (e.g. biological activity) using or routinely modifying assays known in the art and/or assays described herein. For example, one of skill in the art may routinely assay enzyme polypeptides (including fragments and variants) of the invention for activity using assays as described in Examples 38, 39, 46, 47, 55, 60, 61, 62, and 65. Many other enzyme assays are known in the art, and may be useful for demonstrating activities of the polypeptides of the present invention.

[40] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

[41] Table 1A summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further

summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the InventionTABLE 1A

Gene No:	Clone ID NO: Z	Contig ID:	SEQ ID NO: X	ORF (From-To)	AA SEQ ID NO: Y	Predicted Epitopes	Tissue Distribution Library code: count (see Table IV for Library Codes)	Cytologic Band	OMIM Disease Reference(s):
1	HHMMC14	1152250	11	3 - 1088	911	Gln-67 to Pro-75, Glu-166 to Gly-171, Tyr-216 to Glu-225, Ser-306 to Thr-312, Thr-332 to Thr-338.	AR061: 45, AR089: 12, L0777: 28, H0144: 12, L0748: 10, L0766: 9, H0620: 7, L0750: 7, L0581: 7, L0769: 6, L0774: 6, L0749: 5, L0731: 5, H0318: 4, H0510: 4, H0529: 4, L0771: 4, L0775: 4, L0757: 4, H0556: 3, S0360: 3, H0013: 3, H0599: 3, L0770: 3, L0768: 3, L0652: 3, L0655: 3, L0659: 3, S0374: 3, L0751: 3, L0747: 3, L0758: 3, H0341: 2, S0282: 2, H0661: 2, H0662: 2, H0125: 2, S0358: 2,		

H0637: 2, S0278: 2,	H0024: 2, H0188: 2,	H0292: 2, H0031: 2,	S0036: 2, H0264: 2,	H0059: 2, H0494: 2,	H0509: 2, S0344: 2,	L0369: 2, L0761: 2,	L0662: 2, L0807: 2,	L0666: 2, H0547: 2,	S0126: 2, H0435: 2,	S0328: 2, S0027: 2,	S0032: 2, L0744: 2,	L0786: 2, L0593: 2,	L0362: 2, H0423: 2,	H0624: 1, H0171: 1,	T0002: 1, H0583: 1,	H0656: 1, S0116: 1,	H0255: 1, H0192: 1,	S0420: 1, L0005: 1,	S0354: 1, S0376: 1,	S0410: 1, S0007: 1,	S0045: 1, S0046: 1,	S0132: 1, H0357: 1,	H0455: 1, H0592: 1,	H0574: 1, H0492: 1,	H0486: 1, T0114: 1,	S0280: 1, L0021: 1,	H0618: 1, S0010: 1,	S0346: 1, S0049: 1,	L0040: 1, H0545: 1,	H0046: 1, H0150: 1,
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H0246: 1, T0003: 1,
H0373: 1, H0355: 1,
S0628: 1, H0266: 1,
S0334: 1, H0424: 1,
H0417: 1, H0169: 1,
L0455: 1, H0135: 1,
H0163: 1, H0040: 1,
H0087: 1, H0268: 1,
H0413: 1, H0623: 1,
L0351: 1, T0042: 1,
S0438: 1, H0130: 1,
H0646: 1, S0144: 1,
S0142: 1, L0762: 1,
L0796: 1, L0637: 1,
L0374: 1, L0764: 1,
L0773: 1, L0389: 1,
L0806: 1, L0776: 1,
L0657: 1, L0383: 1,
L0382: 1, L0647: 1,
L0663: 1, T0068: 1,
H0520: 1, H0690: 1,
H0683: 1, H0659: 1,
H0658: 1, H0660: 1,
H0672: 1, S0044: 1,
H0134: 1, H0478: 1,
L0754: 1, L0756: 1,
L0779: 1, L0752: 1,
L0753: 1, L0755: 1,
L0759: 1, L0608: 1,
H0668: 1, H0665: 1 and
H0506: 1

2	HSLEQ79	969371	652	3 - 1070	1552	Gln-61 to Pro-69, Glu-160 to Gly-165, Tyr-210 to Glu-219, Ser-300 to Thr-306, Thr-326 to Thr-332.	AR061: 3, AR089: 2 S0001: 1, S0390: 1, S0028: 1 and L0592: 1.		
		1184946	12	674 - 3	912				
		752382	653	1 - 672	1553				
3	HUCME08	1082023	13	2 - 595	913	His-29 to Cys-37, Glu-40 to Pro-49, Glu-140 to Gly-145.	H0318: 3, H0656: 2, H0620: 2, S0420: 1, S0045: 1, H0393: 1, H0357: 1, S0346: 1, H0581: 1, S0628: 1, H0539: 1, L0748: 1, L0750: 1 and L0777: 1.		
		868780	654	2 - 676	1554	His-29 to Cys-37, Glu-40 to Pro-49.			
4	HNGOW33	1152254	14	520 - 1158	914	Ser-1 to Asp-12, Gln-103 to Cys-108, Ser-173 to Lys-182.	AR089: 1, AR061: 1 S0028: 12, S0045: 5, S0144: 4, S0001: 3, S0044: 3, S0031: 3, S0282: 2, H0597: 2, H0617: 2, S0428: 2, S0390: 2, S0037: 2, S0260: 2, H0624: 1, H0171: 1, H0381: 1, H0346: 1, S0132: 1, S0300: 1, S0278: 1, H0318: 1, H0204: 1,		

									S0050: 1, H0271: 1, H0416: 1, H0644: 1, H0181: 1, S0036: 1, H0359: 1, S0150: 1, H0144: 1 and S0146: 1.		
5	HT4GD03	957351 1103896	655 15	268 - 1320 153 - 968	1555 915	Ser-1 to Arg-11. Pro-1 to Leu-6, His-25 to Arg-30, Lys-40 to Lys-46, Thr-95 to Asp-100, Gly-125 to Gly-130, Arg-139 to Pro-144, Lys-179 to Met-187.	AR061: 10, AR089: 5 H0585: 37, H0141: 10, L0809: 6, L0794: 5, L0752: 3, H0135: 2, H0494: 2, L0803: 2, L0749: 2, S6024: 1, S0212: 1, H0255: 1, S0356: 1, H0510: 1, L0761: 1, L0772: 1, L0800: 1, L0773: 1, L0766: 1, L0806: 1, L0782: 1, L0788: 1, H0144: 1, H0659: 1, H0187: 1, L0750: 1, L0777: 1 and L0758: 1.				
6	HAQBZ89	923731 949061	656 16	455 - 967 2 - 325	1556 916	His-14 to Pro-19. Ala-20 to Arg-25.	AR061: 9, AR089: 6 L0659: 4, L0758: 4, L0777: 3, S0360: 2, L0775: 2, L0750: 2, L0731: 2, H0295: 1, S0218: 1, H0255: 1, H0402: 1, L0717: 1, H0411: 1, H0015: 1.				

								H0030: 1, H0644: 1, H0673: 1, H0087: 1, L0770: 1, L0769: 1, L0637: 1, L0761: 1, L0646: 1, L0387: 1, L0766: 1, L0776: 1, L0655: 1, L0789: 1, H0683: 1, S0027: 1, L0748: 1, L0779: 1 and L0757: 1.			
7	HCCCC81	949062	17	139 - 921	917	Gly-8 to Ile-13, Glu-141 to His-146, Glu-186 to Glu-195, Asp-213 to Asn-218.		AR089: 12, AR061: 7 H0583: 1, H0675: 1 and H0457: 1.			
8	HE8PW83	927532	18	1 - 546	918	Glu-69 to Gln-76.		AR089: 0, AR061: 0 L0748: 6, L0749: 6, L0803: 3, L0774: 3, L0775: 3, H0574: 1, H0632: 1, H0013: 1, L0789: 1, L0790: 1, H0144: 1 and L0581: 1.			
9	HE9QQ22	949080	19	3 - 563	919			AR061: 11, AR089: 3 L0748: 3, H0144: 2, H0632: 1 and L0581: 1.			
10	HFPFB39	946170	20	1613 - 462	920	Pro-36 to Lys-46, Pro-56 to Ala-68, Ala-85 to Arg-90, Tyr-191 to Asn-198, Gly-219 to Val-224, Leu-232 to Lys-238,		AR061: 6, AR089: 3 S0010: 4, S0222: 3, H0455: 2, L0803: 2, L0439: 2, L0745: 2, S0282: 1, S0400: 1, H0456: 1, H0441: 1,			

									His-260 to Ala-266.	S0346: 1, H0509: 1, L0769: 1, L0438: 1, L0756: 1 and S0106: 1.			
11	HSDJI44	1151680	21	272 - 2143	921					AR061: 0, AR089: 0 S0045: 6, H0255: 5, S0028: 4, S0031: 2, S0260: 2, H0341: 1, S0278: 1, H0333: 1, H0250: 1, S0050: 1, H0271: 1, H0100: 1, S0216: 1, S0044: 1 and S0390: 1.			
		974784	657	210 - 1847	1557				Ala-324 to Phe-332, Arg-336 to Thr-343, Pro-373 to Arg-384, Lys-424 to Asp-431.				
12	HE9DG38	1181748	22	2 - 994	922				Ala-30 to Lys-45, Ala-71 to Ala-85, Gly-112 to Asn-117, Asn-131 to Gly-140, Ser-143 to Ala-148, Leu-230 to Val-235, Gly-301 to Asn-312.	AR061: 6, AR089: 2 H0052: 3, H0457: 3, H0618: 2, H0622: 2, L0770: 2, L0438: 2, L0439: 2, H0257: 1, L0471: 1, H0428: 1, H0135: 1, H0144: 1, H0519: 1, H0521: 1, L0741: 1, L0756: 1 and H0707: 1.			
		943384	658	1 - 1371	1558				Ala-28 to Lys-43, Ala-69 to Ala-83, Gly-110 to Asn-115, Asn-129 to Gly-138,				

13	HGBAT24	1024746	23	1 - 420	923	Ser-141 to Ala-146.	AR061: 41, AR089: 30 H0014: 2, S0028: 1 and S0031: 1.		
14	HTDAF92	761143	659	1 - 420	1559				
		1181747	24	112 - 1011	924	Leu-71 to Val-76, Gly-142 to Asn-153, Asp-180 to Arg-188, Ser-202 to Asn-212, His-244 to Pro-251, Arg-275 to Ala-280.	AR089: 2, AR061: 1 L0439: 3, S0222: 2, H0543: 2, S0360: 1, H0622: 1, H0063: 1, H0477: 1, T0042: 1, L0369: 1, L0771: 1, L0662: 1, L0659: 1, L0809: 1 and L0786: 1.		
		943385	660	112 - 627	1560	Leu-71 to Val-76, Gly-142 to Asn-153.			
15	HAPSI19	972980	661	718 - 401	1561	Thr-15 to Tyr-20, Ser-54 to Leu-63.			
		668405	25	176 - 397	925	Leu-1 to Tyr-10.	AR089: 389, AR061: 120	19q13.3-q13.4	113900, 126340, 126391, 130410, 134790, 138570, 160900, 173850, 191044, 258501, 600040, 600138, 602225,

16	HADTU18	666268	26	185 - 442	926	Leu-48 to Gln-54.	AR061: 197, AR089: 100		602225
17	HNTEF53	954852	27	33 - 938	927	Pro-45 to Ser-53, Ala-55 to Ala-63, Asp-130 to Leu-136.	AR089: 2, AR061: 1, L0439: 4, L0105: 2, H0271: 2, L0637: 2, L0653: 2, H0519: 2, S0330: 2, H0431: 1, H0052: 1, L0471: 1, H0375: 1, L0763: 1, L0794: 1, L0803: 1, L0774: 1, L0806: 1, L0526: 1, L0809: 1, L0666: 1, L0664: 1 and H0648: 1.		
18	HWLLB11	954849	28	51 - 524	928	Pro-1 to Glu-10, His-60 to Arg-76, Pro-79 to Arg-85, Ala-95 to Ile-101, Glu-124 to Glu-130, Lys-151 to Arg-158.	AR061: 2, AR089: 2, S0358: 2, L0657: 1 and L0601: 1.		
19	HCRQK86	1193068	29	2 - 1339	929	Arg-1 to Gly-7, Pro-19 to Cys-27, Leu-61 to Ala-72, Ser-90 to Ser-96, Thr-126 to Ser-143, Glu-167 to Gln-176, Ile-185 to Ser-193, Phe-249 to Phe-256,	AR061: 1, AR089: 1, L0748: 6, H0013: 3, L0794: 3, L0438: 3, L0747: 3, L0731: 3, L0005: 2, S0360: 2, H0494: 2, L0769: 2, L0766: 2, L0803: 2, L0655: 2, L0756: 2,		

27

20	HOCOT88	933635	30	331 - 1449	930	Glu-162 to Gln-171, Ile-180 to Ser-188, Phe-244 to Phe-251, Ala-255 to Ser-266, Tyr-293 to Lys-299, Ser-306 to Arg-317, Ser-341 to Gly-351, Glu-395 to Ser-406. Ser-13 to Arg-19, Leu-28 to Val-35, Pro-37 to Gly-57, Ser-81 to Pro-87, Ile-102 to Arg-111.	AR061: 1, AR089: 0 L0766: 3, H0341: 2, H0599: 2, H0457: 2, H0169: 2, S0146: 2, H0444: 2, H0445: 2, L0592: 2, H0619: 1, S0222: 1, H0455: 1, H0592: 1, H0486: 1, H0013: 1, S0010: 1, S0665: 1, H0544: 1, L0471: 1, T0042: 1, H0560: 1, H0359: 1, L0662: 1, L0528: 1, L0529: 1, L0543: 1, L0438: 1, H0435: 1, H0660: 1, H0518: 1, S0044: 1, L0439: 1, L0745: 1, L0753: 1, S0260: 1, L0594: 1, H0542: 1, H0423: 1 and H0422: 1.
21	HEI EE11	926930	31	53 - 625	931	Phe-21 to Lys-27.	AR061: 1, AR089: 1

22	HOUGD29	1204714	32	199 - 1821	932	Arg-9 to Gln-17, Ile-33 to Asn-39, Gln-93 to Ser-104, Asp-141 to Leu-155, Ser-224 to Asn-234, Asn-243 to Lys-248, Ser-308 to Gln-320, Thr-350 to Glu-357, Ser-384 to Thr-390, Asp-435 to Ser-447, Ala-480 to Lys-487, Lys-496 to Leu-508, Ser-519 to Val-528, Ser-533 to Gln-541.	S0045: 1 and H0457: 1. AR061: 6, AR089: 5 L0770: 4, L0789: 3, L0439: 3, L0750: 3, L0641: 2, L0747: 2, L0758: 2, S0040: 1, H0575: 1, T0010: 1, H0087: 1, S0422: 1, L0803: 1, L0375: 1, L0776: 1, L0659: 1, L0783: 1, H0144: 1, L0352: 1, H0684: 1, H0660: 1, S0027: 1, L0777: 1 and H0445: 1.		
23	HSIGN57	910078	33	199 - 909 2 - 760	1563 933	Arg-9 to Leu-15. Val-10 to Gly-16, Met-19 to Val-34.	AR061: 2, AR089: 1 H0229: 1, H0590: 1, S0049: 1, H0014: 1, H0560: 1, L0439: 1 and H0543: 1.		
24	HTEPE35	948475	34	839 - 78	934	Tyr-1 to Lys-8, Phe-19 to Ser-24, Thr-28 to Ser-34, Pro-54 to Trp-70.	AR061: 4, AR089: 1 L0758: 7, L0768: 2, H0616: 1 and L0151: 1.		
25	HUFDB74	1227205	35	2 - 562	935	Gln-43 to Thr-58, Asn-74 to His-79, Gly-109 to Trp-114, Asp-136 to Phe-145.	AR061: 1, AR089: 1 H0575: 2, L0754: 2, H0599: 1, T0048: 1, L0163: 1, H0051: 1, H0188: 1, H0379: 1,		

									L0438: 1, H0670: 1, H0672: 1, L0439: 1, L0747: 1, S0260: 1, L0591: 1 and H0506: 1.		
		901451	664	2 - 412	1564	Gln-43 to Thr-58, Asn-74 to His-79, Gly-109 to Trp-114.					
26	HBXAB33	1229908	36	3 - 581	936	Asp-1 to Ala-6, Pro-25 to Pro-30.			AR089: 8, AR061: 4 L0748: 35, L0747: 15, H0052: 11, L0766: 11, L0439: 10, L0740: 9, L0595: 9, H0556: 8, H0599: 6, S0010: 6, S0418: 5, H0318: 5, H0050: 5, H0673: 5, H0591: 5, L0770: 5, L0593: 5, H0265: 4, S0046: 4, H0431: 4, H0574: 4, H0013: 4, H0083: 4, S0022: 4, L0776: 4, H0144: 4, L0746: 4, L0750: 4, L0777: 4, L0752: 4, L0731: 4, L0604: 4, L0603: 4, S0420: 3, S0354: 3, H0261: 3, H0331: 3, H0156: 3, H0046: 3, H0373: 3, H0266: 3, H0090: 3, H0551: 3, H0413: 3,		

	H0561: 3, L0775: 3, L0806: 3, L0509: 3, L0663: 3, H0435: 3, S0152: 3, H0171: 2, S0116: 2, S0376: 2, H0393: 2, L0717: 2, S0222: 2, L0623: 2, T0039: 2, H0024: 2, H0014: 2, T0010: 2, H0288: 2, S0250: 2, S0003: 2, H0031: 2, L0456: 2, H0135: 2, H0038: 2, H0616: 2, S0038: 2, H0560: 2, H0509: 2, H0646: 2, L0769: 2, L0646: 2, L0648: 2, L0662: 2, L0768: 2, L0774: 2, L0651: 2, L0659: 2, L0666: 2, L0664: 2, L0438: 2, S0126: 2, H0539: 2, H0521: 2, S0037: 2, S3014: 2, S0028: 2, L0742: 2, L0756: 2, L0758: 2, L0759: 2, L0596: 2, L0588: 2, L0591: 2, L0592: 2, L0485: 2, L0581: 2, L0599: 2, L0594: 2, S0192: 2, H0542: 2, H0543: 2					
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H0624: 1, S0040: 1, S0114: 1, T0049: 1, H0341: 1, S0001: 1, H0664: 1, H0458: 1, H0125: 1, S0356: 1, S0360: 1, S0045: 1, H0619: 1, S6026: 1, H0351: 1, S0278: 1, H0391: 1, H0409: 1, H0587: 1, H0632: 1, H0244: 1, H0250: 1, H0069: 1, H0575: 1, S0346: 1, S0049: 1, H0597: 1, H0544: 1, H0009: 1, H0178: 1, H0123: 1, L0471: 1, S0362: 1, L0163: 1, N0007: 1, S0051: 1, H0290: 1, S0214: 1, H0428: 1, H0039: 1, H0622: 1, T0006: 1, H0644: 1, H0181: 1, S0364: 1, L0455: 1, S0036: 1, T0067: 1, H0380: 1, H0264: 1, H0488: 1, H0623: 1, H0059: 1, H0494: 1, H0625: 1, S0150: 1, S0344: 1, S0210: 1, S0002: 1, S0426: 1, L0371: 1, L0761: 1.

27	HMABF84	11198479	957228	665	2424 - 1081	1565	Lys-70 to Met-78, Tyr-85 to Lys-91, Gln-195 to Cys-205, Pro-234 to Lys-245, Gly-270 to Asp-275, Asp-315 to Ser-324, Pro-352 to Gln-357, Leu-380 to Trp-389.	L0642: 1, L0764: 1, L0771: 1, L0498: 1, L0497: 1, L0804: 1, L0542: 1, L0782: 1, L0383: 1, L0809: 1, L0647: 1, L0665: 1, S0374: 1, H0547: 1, H0519: 1, H0690: 1, H0670: 1, H0660: 1, H0134: 1, S0432: 1, L0755: 1, S0031: 1, L0608: 1, L0366: 1, S0011: 1 and S0026: 1.	
							Pro-21 to Arg-28, Arg-56 to Thr-63, Tyr-84 to Asp-89.	AR061: 3, AR089: 1 H0617: 4, S0212: 2, S0360: 2, S0144: 2, L0803: 2, H0587: 1, H0013: 1, H0046: 1, H0616: 1, H0100: 1, S0422: 1, H0529: 1, L0774: 1, L0809: 1, L0790: 1, L0791: 1.	

							L0748: 1 and L0747: 1.		
		944629	666	1 - 465	1566	Arg-14 to Thr-21, Tyr-42 to Asp-47.			
28	HPTVF17	1150836	38	712 - 245	938	Gly-1 to Gln-11, Ser-24 to Cys-33, Thr-37 to Gly-46, Thr-51 to Thr-63. Pro-10 to Pro-17, Cys-41 to Pro-50, Asn-64 to Arg-73, Ser-81 to Arg-87, Glu-93 to Pro-100.	AR061: 8, AR089: 4 H0424: 1 and L0595: 1.		
		936688	667	2 - 679	1567				
29	HSDIC55	1197407	39	570 - 1	939	Leu-29 to Gly-40, Tyr-93 to Ile-100. Tyr-28 to Val-37, Gln-39 to Met-44, Leu-52 to Asp-60.	AR089: 0, AR061: 0		
		506582	668	1 - 381	1568				
30	HSDIL35	1228138	40	2 - 313	940		AR089: 1, AR061: 0 H0598: 1, S0028: 1 and S0260: 1.		
		656370	669	3 - 371	1569				
31	HTXSM05	1104951	41	2 - 565	941	Pro-48 to Gly-53, Pro-88 to Ser-94, Gly-103 to Ser-108, Pro-141 to Gln-150. Pro-48 to Gly-53, Pro-88 to Ser-94, Gly-103 to Gly-111.	AR061: 10, AR089: 5 H0264: 2, H0556: 1, S0366: 1, S3012: 1 and L0485: 1.		
		958447	670	2 - 424	1570				
32	HYAAH23	1032585	42	322 - 606	942	Ser-39 to Thr-45, Thr-65 to Thr-71.	AR061: 23, AR089: 15 L0777: 28, H0257: 19,	9q12	602014

	H0144: 12, L0748: 10, L0766: 9, H0620: 7, L0769: 7, L0750: 7, L0581: 7, H0559: 6, L0774: 6, L0749: 6, H0529: 5, L0771: 5, L0751: 5, L0731: 5, L0757: 5, H0318: 4, H0510: 4, L0775: 4, L0744: 4, H0556: 3, S0360: 3, H0256: 3, H0013: 3, H0599: 3, H0266: 3, H0059: 3, L0770: 3, L0662: 3, L0768: 3, L0652: 3, L0655: 3, L0659: 3, L0666: 3, S0374: 3, L0747: 3, L0758: 3, L0595: 3, H0341: 2, S0282: 2, H0661: 2, H0662: 2, H0125: 2, S0358: 2, H0637: 2, S0278: 2, H0024: 2, H0373: 2, H0188: 2, H0292: 2, H0031: 2, S0036: 2, H0264: 2, H0494: 2, H0509: 2, S0144: 2, S0344: 2, L0369: 2, L0761: 2, L0807: 2, L0663: 2, H0547: 2, S0126: 2.						
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H0040: 1, H0087: 1, H0268: 1, H0413: 1, H0623: 1, L0351: 1, T0042: 1, S0438: 1, H0130: 1, H0646: 1, S0142: 1, S0002: 1, L0762: 1, L0796: 1, L0637: 1, L0800: 1, L0374: 1, L0764: 1, L0773: 1, L0767: 1, L0794: 1, L0389: 1, L0806: 1, L0776: 1, L0657: 1, L0658: 1, L0383: 1, L0382: 1, L0647: 1, L0789: 1, L0664: 1, L0565: 1, T0068: 1, H0520: 1, H0690: 1, H0683: 1, H0659: 1, H0658: 1, H0660: 1, H0672: 1, H0651: 1, H0521: 1, S0044: 1, H0134: 1, H0478: 1, L0439: 1, L0754: 1, L0756: 1, L0779: 1, L0752: 1, L0753: 1, L0755: 1, L0759: 1, L0608: 1, H0668: 1, H0665: 1, S0276: 1, S0196: 1, H0506: 1 and H0352: 1.							
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33	HTPDX13	1134372	43	2 - 922	943		AR089: 0, AR061: 0 H0549: 1, H0485: 1, H0039: 1, H0553: 1, H0040: 1 and S0126: 1.		
		948419	671	2 - 922	1571				
34	HAIHE43	1172244	44	2 - 376	944		AR089: 20, AR061: 8 H0599: 2, L0759: 2, H0556: 1, H0638: 1, S0418: 1, S6022: 1, L0021: 1, S0010: 1, H0266: 1, H0553: 1, H0644: 1, L0763: 1, L0641: 1, L0766: 1, L0805: 1, L0655: 1, H0539: 1, S0028: 1 and L0777: 1.		
		966830	672	2 - 376	1572				
35	HAJAV28	948630	45	3 - 464	945	Pro-1 to Ala-12.	AR089: 3, AR061: 1 L0747: 12, L0755: 12, L0766: 9, L0438: 9, L0754: 7, H0046: 6, L0751: 6, L0752: 6, H0068: 5, L0775: 5, L0439: 5, S0010: 4, H0547: 4, S0152: 4, L0740: 4, L0779: 4, L0759: 4, H0591: 3, L0771: 3, L0662: 3, L0774: 3, L0666: 3, S0028: 3, L0748: 3,	1q21-q25	104770, 107300, 107670, 110700, 131210, 135940, 136132, 145001, 146790, 150292, 152445, 152445, 159001,

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									H0674: 1, S0364: 1, H0090: 1, H0040: 1, H0551: 1, T0067: 1, H0268: 1, H0100: 1, H0494: 1, H0560: 1, H0561: 1, H0633: 1, L0762: 1, L0763: 1, L0638: 1, L0772: 1, L0773: 1, L0521: 1, L0768: 1, L0794: 1, L0803: 1, L0809: 1, L0545: 1, L0664: 1, L0665: 1, H0144: 1, S0126: 1, H0660: 1, H0672: 1, S0378: 1, S0380: 1, S0350: 1, H0555: 1, H0436: 1, H0540: 1, S0390: 1, S0206: 1, S0032: 1, L0741: 1, L0749: 1, L0786: 1, L0777: 1, L0758: 1, S0026: 1 and H0506: 1.					
36	HAPOR59	712955	46	3 - 368	946	Ala-4 to Glu-11, Lys-62 to Arg-71.	AR089: 29, AR061: 9 H0575: 1 and H0083: 1.							
37	HBIBF78	1123470	47	879 - 640	947		AR061: 6, AR089: 3 S0049: 1 and L0439: 1.							
		772797	673	45 - 206	1573	Lys-42 to Ser-49.								
38	HCDAJ15	1091635	48	176 - 388	948	Arg-12 to Thr-20,	AR089: 8, AR061: 8							

									H0251: 2 and S0392: 1.		
39	HCE1S21	557243 671209	674 49	2 - 190 1 - 297	1574 949				His-55 to Lys-61. Glu-9 to Asp-14.	AR061: 5, AR089: 2 H0052: 1, L0581: 1 and L0366: 1. AR089: 24, AR061: 15 H0052: 2, L0759: 2, S0376: 1, H0333: 1, S0388: 1, L0637: 1, L0636: 1, L0742: 1 and L0439: 1.	
40	HCE3J64	951228	50	3 - 593	950				Thr-1 to Lys-8, Lys-26 to Asp-33, Gln-60 to Trp-70, Phe-99 to Lys-106, Asp-126 to Asn-137, Arg-139 to Glu-145, Met-157 to Tyr-164, Asn-167 to Arg-174.		
41	HCFCV92	1124565	51	922 - 1143	951				Gly-68 to Leu-74.	AR089: 2, AR061: 2 L0766: 3, H0521: 2, H0422: 2, H0661: 1, H0369: 1, H0687: 1, L0646: 1, L0655: 1, L0665: 1, H0519: 1, H0436: 1 and L0779: 1.	
42	HCFLI54	934216 921382	675 52	413 - 655 259 - 522	1575 952					AR089: 1, AR061: 0 L0439: 6, L0748: 5, L0758: 4, L0591: 4, L0766: 3, L0805: 3, L0438: 3, H0102: 2, L0666: 2, L0740: 2, H0423: 2, S0360: 1, S0046: 1, H0393: 1, H0411: 1, H0391: 1,	

43	HCFND04	1155680	53	1 - 1146	953					H0586: 1, H0156: 1, H0575: 1, H0023: 1, H0266: 1, H0267: 1, H0622: 1, T0006: 1, H0674: 1, S0386: 1, L0770: 1, L0638: 1, L0373: 1, L0662: 1, L0776: 1, L0518: 1, L0809: 1, L0663: 1, H0684: 1, H0435: 1, H0648: 1, H0672: 1, H0436: 1, H0478: 1, L0744: 1 and L0747: 1. AR089: 7, AR061: 3 S0474: 1, T0067: 1, L0805: 1, L0777: 1, L0780: 1 and H0423: 1.			
									Pro-2 to Leu-23, Gln-54 to Gly-62, Glu-68 to Asn-80, Glu-82 to Pro-94, Gln-100 to Thr-108, Pro-114 to Lys-123, Pro-128 to Lys-137, Leu-143 to Lys-151, Pro-157 to Gly-170, Lys-173 to Lys-185, Asp-193 to Glu-211, Gly-236 to Met-241, Asp-298 to Trp-304, Tyr-306 to Ile-314, Thr-322 to Tyr-331, Thr-371 to Thr-376.	Ile-10 to Cys-21,			
										873441	676	273 - 1145	1576

44	HCHMV63	1190101	54	889 - 2	954	Thr-24 to Gln-60. Gly-1 to Trp-6, Pro-9 to Asp-18, Val-56 to Thr-66, Pro-73 to Trp-79, Ala-82 to Trp-102, Gln-108 to Cys-119, Ser-145 to Arg-166, Arg-239 to Asn-247.	AR089: 2, AR061: 1 S0412: 12, L0758: 5, L0743: 4, L0748: 4, H0545: 3, L0769: 3, L0665: 3, H0341: 2, S0360: 2, H0457: 2, H0644: 2, H0032: 2, S0144: 2, L0762: 2, L0766: 2, L0774: 2, L0530: 2, H0436: 2, L0747: 2, L0759: 2, L0581: 2, H0352: 2, H0657: 1, H0656: 1, S0282: 1, H0484: 1, H0663: 1, S0358: 1, H0370: 1, L0586: 1, H0013: 1, S0010: 1, H0596: 1, H0594: 1, H0606: 1, H0135: 1, H0090: 1, H0616: 1, H0641: 1, H0633: 1, L0770: 1, L0771: 1, L0662: 1, L0767: 1, L0768: 1, L0803: 1, L0805: 1, L0509: 1, L0653: 1, L0515: 1, L0659: 1, H0520: 1, H0435: 1, H0659: 1, H0521: 1, H0696: 1,
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								S3014: 1, S0027: 1, L0439: 1, L0740: 1, L0749: 1, L0756: 1, S0260: 1 and H0423: 1.		
45	HCWDL45	666798	677	2 - 262	1577	His-48 to Thr-54.		AR089: 16, AR061: 4 H0305: 6 and S0052: 1.		
46	HCWEI19	889416	55	118 - 282	955	Ala-33 to Ile-42.		AR089: 4, AR061: 2 H0305: 2		
		1125258	56	116 - 448	956	Lys-1 to Ser-7, Pro-71 to Gly-81.				
		948690	678	178 - 309	1578					
47	HCWKB72	1224131	57	1527 - 3206	957	Leu-73 to Lys-87, Met-91 to Pro-171, Glu-198 to Ser-298, Ser-306 to Ser-336, Ser-338 to Ser-373, Pro-379 to Val-407, Ser-410 to Gly-418, Ser-425 to His-458, Val-464 to Arg-541.	AR061: 2, AR089: 2 H0305: 4, H0266: 3, H0624: 2, H0618: 2, S0036: 2, H0040: 2, T0041: 2, L0749: 2, L0777: 2, H0265: 1, H0556: 1, S0134: 1, H0013: 1, H0069: 1, H0599: 1, H0575: 1, H0421: 1, T0110: 1, H0188: 1, H0428: 1, H0135: 1, H0634: 1, H0488: 1, H0056: 1, H0623: 1, S0038: 1, S0386: 1, H0100: 1, T0042: 1, L0766: 1, H0521: 1, H0522: 1, H0436: 1, S3014: 1, S0027: 1, L0779: 1, S0260: 1, L0588: 1,			

							L0366: 1 and L0462: 1.		
48	HDDAF49	676007 1125713	679 58	101 - 193 549 - 298	1579 958		AR061: 9, AR089: 3 H0339: 1		
49	HDPGQ74	911314 691163	680 59	144 - 320 3 - 320	1580 959	Glu-15 to Ser-24. Asp-19 to Leu-24.	AR061: 0, AR089: 0 H0551: 5, H0545: 4, H0521: 4, L0748: 4, L0790: 3, S0278: 2, H0586: 2, H0333: 2, H0632: 2, H0052: 2, H0023: 2, S0250: 2, S0142: 2, S0426: 2, H0529: 2, L0565: 2, H0547: 2, L0439: 2, H0170: 1, H0685: 1, H0295: 1, H0458: 1, S0418: 1, L0534: 1, S0132: 1, H0587: 1, H0485: 1, H0544: 1, H0081: 1, L0471: 1, S0050: 1, S0388: 1, H0510: 1, H0286: 1, H0428: 1, H0032: 1, H0124: 1, H0488: 1, L0065: 1, H0538: 1, S0002: 1, L0770: 1, L0769: 1, L0646: 1, L0644: 1, L0773: 1, L0363: 1, L0774: 1.		

46

51	HDP1X67	1172240	61	3 - 470	961	Gln-19 to Gly-24, Gln-34 to Leu-42, Gln-44 to Glu-49	AR089: 3, AR061: 1 L0756: 3, H0622: 2, L0751: 2, H0624: 1	L0698: 2, H0149: 1, H0686: 1, S0212: 1, H0255: 1, H0637: 1, S0046: 1, H0411: 1, S0278: 1, H0599: 1, H0251: 1, H0545: 1, H0457: 1, H0024: 1, H0014: 1, H0328: 1, H0553: 1, H0644: 1, H0598: 1, H0634: 1, H0268: 1, H0056: 1, L0564: 1, S0344: 1, S0002: 1, S0426: 1, L0770: 1, L0372: 1, L0641: 1, L0645: 1, L0648: 1, L0767: 1, L0649: 1, L0389: 1, L0388: 1, L0803: 1, L0654: 1, L0665: 1, S0052: 1, S0053: 1, S0216: 1, H0658: 1, H0672: 1, H0518: 1, H0522: 1, H0696: 1, S0406: 1, L0750: 1, L0752: 1, H0445: 1, L0596: 1, S0458: 1 and H0506: 1.		
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							Gln-56 to Glu-61, Leu-76 to Phe-85, Cys-97 to Arg-102.				H0265: 1, S0402: 1, H0650: 1, S0444: 1, H0497: 1, H0643: 1, H0632: 1, H0673: 1, H0038: 1, H0646: 1, S0002: 1, L0764: 1, L0766: 1, L0803: 1, L0776: 1, L0790: 1, L0666: 1, H0520: 1, S0152: 1, H0521: 1, H0134: 1, L0743: 1, L0777: 1 and H0543: 1.	
52	HDPXN01		954385	681	2 - 334	1581	Gln-11 to Glu-16, Leu-31 to Phe-40.				AR089: 9, AR061: 4 L0794: 5, L0439: 2, L0747: 2, H0521: 1, L0779: 1, L0777: 1 and L0594: 1.	
53	HDQFT77		915919 1136137	682 63	69 - 230 2 - 958	1582 963	Ser-48 to Ser-53. Pro-13 to Leu-23, Glu-39 to Gly-51, Ser-54 to Glu-65, Ala-77 to Gly-84, Gln-90 to Val-96, Arg-104 to Gly-113, Thr-120 to Cys-125, Asn-154 to Ser-160, Glu-162 to Val-168, Leu-247 to Gln-252,				AR089: 16, AR061: 8 L0803: 5, L0655: 3, L0747: 3, L0779: 3, L0771: 2, L0766: 2, L0775: 2, L0666: 2, S0126: 2, L0755: 2, L0758: 2, H0656: 1, H0351: 1, H0586: 1, H0559: 1, H0598: 1, H0038: 1, L0761: 1,	

54	HE2FR50	508498	64	50 - 391	964	<p>Phe-286 to Arg-294, Pro-296 to Tyr-301, Asp-308 to Ser-317.</p> <p>Glu-11 to Gly-23, Ser-26 to Glu-37, Ala-49 to Gly-56, Gln-62 to Val-68, Arg-76 to Gly-85, Thr-92 to Cys-97, Asn-126 to Ser-132, Glu-134 to Val-140, Leu-219 to Gln-224, Phe-258 to Arg-266, Pro-268 to Tyr-273, Asp-280 to Ser-289.</p>	<p>L0804: 1, L0774: 1, L0805: 1, H0521: 1, L0750: 1 and L0759: 1.</p>		
55	HE2SN25	1151226	65	1239 - 1024	965	<p>Leu-7 to Lys-13.</p>	<p>AR061: 10, AR089: 3 L0659: 3, L0766: 2, S0330: 2, L0731: 2, L0758: 2, H0171: 1, H0650: 1, S0356: 1, H0675: 1, S0182: 1, H0184: 1, H0009: 1, H0039: 1, H0038: 1, H0560: 1, L0770: 1, L0637: 1, L0655: 1, L0666: 1, H0659: 1, S0328: 1, H0518: 1, H0521: 1, L0752: 1, S0260: 1 and L0588: 1.</p>		
55	HE2SN25	1151226	65	1239 - 1024	965	<p>Leu-7 to Lys-13.</p>	<p>AR061: 4, AR089: 3</p>		

										L0439: 2, H0624: 1, H0171: 1, S0114: 1, L0774: 1, H0539: 1 and L0752: 1.		
56	HE8AE26	948687	684	134 - 277	1584	Thr-1 to His-10.				AR089: 11, AR061: 10 H0013: 2 and H0427: 1.		
		1147168	66	247 - 597	966	Ser-74 to Ala-81.						
		851514	685	34 - 210	1585							
57	HEBGK01	963673	67	453 - 109	967	Gly-48 to Gly-54.				AR061: 0, AR089: 0 H0617: 7, H0483: 1, S0007: 1, S0051: 1, H0182: 1, H0606: 1, L0769: 1, L0761: 1 and H0547: 1.		
58	HEFMB30	691516	68	51 - 221	968					AR061: 1, AR089: 0 L0804: 2, S0402: 1, H0648: 1, L0748: 1 and L0749: 1.		
59	HEOPE58	851009	69	257 - 421	969	Phe-28 to Val-36, Phe-44 to Pro-49.				AR089: 1, AR061: 0 H0457: 4		
60	HETBR74	948667	70	216 - 479	970	Leu-78 to Cys-88.				AR061: 8, AR089: 6 H0170: 1, S0045: 1, H0619: 1, H0046: 1, L0761: 1, L0754: 1 and S0026: 1.		
61	HFCAG94	1111177	71	1010 - 669	971					AR089: 16, AR061: 7 H0009: 1 and H0520: 1.		
		735763	686	82 - 180	1586							

62	HFPHR82	957528	72	1592 - 273	972	Ile-256 to Val-269, Gln-296 to Gln-301, Ile-316 to Leu-322, Glu-351 to Leu-359, Ser-395 to Arg-406, Gly-425 to Leu-431.	AR089: 3, AR061: 1 L0747: 12, L0755: 12, L0766: 9, L0438: 9, L0754: 7, H0046: 6, L0751: 6, L0752: 6, H0068: 5, L0775: 5, L0439: 5, S0010: 4, H0547: 4, S0152: 4, L0740: 4, L0779: 4, L0759: 4, H0591: 3, L0771: 3, L0662: 3, L0774: 3, L0666: 3, S0028: 3, L0748: 3, L0756: 3, L0731: 3, L0757: 3, H0624: 2, S0045: 2, H0619: 2, S0222: 2, S0049: 2, H0052: 2, H0615: 2, S0036: 2, T0041: 2, H0509: 2, S0002: 2, S0426: 2, L0769: 2, L0776: 2, L0659: 2, H0521: 2, H0707: 2, L0594: 2, L0362: 2, S0011: 2, H0170: 1, H0171: 1, H0685: 1, S0040: 1, T0049: 1, H0657: 1, S0001: 1, H0638: 1, S0358: 1, S0360: 1, S0408: 1, H0637: 1, S0007: 1,	11q21-q25	104770, 107300, 107670, 110700, 131210, 135940, 136132, 145001, 146790, 150292, 152445, 152445, 159001, 173610, 174000, 179755, 182860, 182860, 182860, 191315, 208250, 230800, 230800, 233710, 266200, 600897, 600995, 601105, 601412, 601518, 601652,
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					S0132: 1, S6022: 1, H0550: 1, H0431: 1, H0455: 1, H0574: 1, H0486: 1, T0114: 1, H0250: 1, H0069: 1, H0156: 1, L0105: 1, H0597: 1, H0546: 1, H0545: 1, H0050: 1, L0163: 1, H0594: 1, H0266: 1, H0290: 1, S0214: 1, H0328: 1, H0688: 1, H0622: 1, H0032: 1, H0673: 1, H0674: 1, S0364: 1, H0090: 1, H0040: 1, H0551: 1, T0067: 1, H0268: 1, H0100: 1, H0494: 1, H0560: 1, H0561: 1, H0633: 1, L0762: 1, L0763: 1, L0638: 1, L0772: 1, L0773: 1, L0521: 1, L0768: 1, L0794: 1, L0803: 1, L0809: 1, L0545: 1, L0664: 1, L0665: 1, H0144: 1, S0126: 1, H0660: 1, H0672: 1, S0378: 1, S0380: 1, S0350: 1, H0555: 1, H0436: 1, H0540: 1, S0390: 1.	602491
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								S0206: 1, S0032: 1, L0741: 1, L0749: 1, L0786: 1, L0777: 1, L0758: 1, S0026: 1 and H0506: 1.			
63	HHFOO84	857780	73	78 - 275	973			AR089: 7, AR061: 4 S0344: 3, H0539: 2, L0758: 2, H0685: 1, H0657: 1, H0656: 1, S0116: 1, H0341: 1, H0645: 1, H0549: 1, H0331: 1, H0574: 1, T0039: 1, H0318: 1, H0050: 1, H0135: 1, H0641: 1, L0374: 1, L0662: 1, L0768: 1, L0803: 1, L0775: 1, L0776: 1, L0368: 1, L0665: 1, H0689: 1, H0435: 1, H0659: 1, H0134: 1, L0749: 1, L0779: 1, L0759: 1 and S0194: 1.			
64	HISAM68	1125189	74	590 - 3	974	Arg-9 to Leu-28, Ser-108 to Thr-113, Gly-152 to Gly-159, Pro-170 to Ser-184.		AR089: 1, AR061: 0 L0803: 6, L0774: 2, H0056: 1, L0761: 1, L0800: 1, L0766: 1, L0806: 1 and H0539: 1.			
		868785	687	1 - 498	1587	Ser-84 to Thr-89, Gly-128 to Gly-135,					

65	HLHDD45	942901	75	21 - 230	975	Pro-146 to Ser-160. Lys-1 to Gly-9, Ser-30 to Gly-36.	AR089: 33, AR061: 7 H0556: 3, H0208: 3, H0619: 3, H0050: 3, L0471: 3, H0179: 3, H0644: 3, S0344: 3, H0521: 3, L0439: 3, S0420: 2, S0360: 2, H0599: 2, H0264: 2, H0280: 2, S0210: 2, H0547: 2, H0658: 2, L0750: 2, L0731: 2, L0588: 2, L0604: 2, H0543: 2, H0265: 1, T0002: 1, H0140: 1, S0114: 1, H0341: 1, S0001: 1, H0669: 1, H0662: 1, H0306: 1, S0418: 1, H0580: 1, L0717: 1, H0549: 1, H0453: 1, H0592: 1, H0497: 1, H0632: 1, T0039: 1, T0112: 1, H0575: 1, H0036: 1, H0309: 1, H0544: 1, H0172: 1, H0123: 1, H0620: 1, H0024: 1, H0051: 1, H0188: 1, H0615: 1, H0604: 1, H0031: 1, L0456: 1,		
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									H0124: 1, H0376: 1, S0036: 1, H0059: 1, H0100: 1, T0041: 1, T0042: 1, S0150: 1, H0646: 1, H0538: 1, L0637: 1, L0551: 1, L0803: 1, L0659: 1, L0789: 1, L0663: 1, L0438: 1, H0520: 1, H0519: 1, S0126: 1, H0689: 1, H0651: 1, H0539: 1, S0152: 1, S0028: 1, L0748: 1, L0777: 1, L0753: 1, H0343: 1, L0591: 1, L0592: 1, L0593: 1, H0423: 1, H0422: 1, H0506: 1 and H0008: 1.			
66	HMMAB49	1087684	76	462 - 160	976	Lys-8 to Ser-13, Lys-52 to Ser-69, Cys-87 to His-93.			AR089: 53, AR061: 4 H0444: 2			
		462502	688	1 - 204	1588							
67	HMSG027	683031	77	236 - 3	977	Leu-20 to Gly-25, Pro-28 to His-40.			AR089: 11, AR051: 7, AR061: 1, AR054: 0 H0638: 1, H0046: 1, S0112: 1 and S0002: 1.			
		943946	689	127 - 462	1589	Ser-1 to Leu-6, His-54 to Cys-61.						
		947911	690	55 - 171	1590	Phe-1 to Arg-12.						
68	HNHAM52	1125710	78	880 - 539	978				AR061: 2, AR089: 1			

									H0457: 1, H0674: 1, L0803: 1, S0053: 1, L0756: 1 and L0592: 1.		
69	HNHEQ86	457010	691	12 - 131	1591	Arg-1 to Asp-6, Glu-26 to Ser-33.			AR061: 0, AR089: 0 S6024: 1, S0001: 1, S0053: 1, S0216: 1, S0028: 1 and S0260: 1.		
70	HNHHF46	1123883	80	1348 - 1040	980				AR061: 4, AR089: 4 L0748: 7, L0774: 2, S0216: 2, L0749: 2, H0455: 1, S0038: 1, S0464: 1, L0637: 1, L0804: 1, L0789: 1 and S0053: 1.		
71	HOECV83	859822	692	3 - 284	1592				AR061: 3, AR089: 2 S0354: 2, L0438: 2, L0750: 2, L0586: 1, H0581: 1, H0052: 1, H0009: 1, L0471: 1, L0179: 1, S0003: 1, L0055: 1, L0655: 1, L0526: 1, S0126: 1, H0521: 1 and S0424: 1.		
		1123893	81	1076 - 1456	981	Pro-53 to Glu-63, Ser-105 to Glu-111.					
72	HORBO54	653276	693	198 - 389	1593				AR061: 4, AR089: 2 L0758: 4, H0556: 3, H0657: 3, H0435: 3,		
		870674	82	115 - 549	982						

					L0749: 3, L0777: 3, H0677: 3, S0045: 2, H0619: 2, H0586: 2, H0032: 2, H0616: 2, L0772: 2, H0701: 2, H0547: 2, S0328: 2, H0543: 2, S0040: 1, S6024: 1, H0295: 1, H0650: 1, S0116: 1, H0661: 1, H0664: 1, S0444: 1, H0580: 1, S0132: 1, S0278: 1, H0486: 1, H0013: 1, H0069: 1, H0427: 1, H0004: 1, H0530: 1, H0050: 1, H0292: 1, T0006: 1, H0553: 1, H0181: 1, L0455: 1, H0038: 1, H0413: 1, T0042: 1, H0494: 1, H0561: 1, H0509: 1, S0344: 1, S0210: 1, L0768: 1, H0144: 1, L0438: 1, H0520: 1, H0519: 1, H0593: 1, H0539: 1, H0521: 1, H0522: 1, H0134: 1, H0555: 1, S0028: 1, L0743: 1, L0740: 1, L0752: 1, L0755: 1, L0759: 1, H0445: 1.				
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						L0803: 1 and S0031: 1.		
77	HSDIM56	947918 948669	697 87	1 - 591 3 - 755	1597 987	Ala-155 to Glu-160. Val-174 to Pro-179, Pro-192 to Ile-207.	AR089: 1, AR061: 1 S0028: 3, S0428: 2, S0282: 1, S0045: 1, S0132: 1, S0222: 1, H0416: 1, S0052: 1, S0152: 1 and S0260: 1.	
78	HSICX21	531267	88	223 - 378	988	Asn-5 to His-12.	AR089: 2, AR061: 0 H0036: 2	
79	HSIDS82	531248	89	146 - 301	989	His-28 to Gln-36.	AR061: 6, AR089: 3 H0036: 2, H0619: 1, H0050: 1 and L0792: 1.	
80	HSNAH21	571314	90	64 - 249	990	Ser-2 to Arg-7, Arg-22 to Pro-28.	AR061: 3, AR089: 1 L0659: 7, L0777: 7, S0358: 6, H0486: 6, H0622: 6, S0360: 4, L0662: 4, H0013: 3, H0144: 3, S0328: 3, L0751: 3, L0731: 3, H0624: 2, H0619: 2, H0328: 2, H0163: 2, L0520: 2, L0764: 2, L0747: 2, S0116: 1, S0356: 1, S0376: 1, H0431: 1, H0600: 1, H0632: 1, H0244: 1, H0599: 1, H0123: 1, H0050: 1, H0051: 1, S0250: 1, H0688: 1,	

81	HSODC08	966264	91	1334 - 222	991	Gln-36 to Asp-41, Ser-73 to Glu-82, Phe-85 to Arg-98, Leu-170 to Glu-176, Lys-226 to Asp-239, Gly-285 to Leu-297, Asp-327 to Glu-339, Glu-343 to Leu-348.	AR089: 5, AR061: 1 H0038: 5, L0748: 5, L0777: 5, L0766: 4, L0769: 3, L0756: 3, L0759: 3, S6028: 2, H0271: 2, L0776: 2, H0435: 2, L0754: 2, L0747: 2, L0779: 2, L0752: 2, L0758: 2, H0595: 2, L0596: 2, H0393: 1, H0431: 1, H0486: 1, H0427: 1, H0004: 1, H0318: 1, H0085: 1, H0546: 1, L0471: 1, S0022: 1, H0252: 1, H0644: 1, H0673: 1, H0674: 1, H0124: 1, H0616: 1,	H0039: 1, H0090: 1, H0591: 1, H0040: 1, H0102: 1, S0150: 1, H0647: 1, H0646: 1, L0640: 1, L0763: 1, L0768: 1, L0649: 1, L0806: 1, L0793: 1, L0666: 1, H0690: 1, H0684: 1, H0658: 1, H0648: 1, L0779: 1, L0780: 1, L0759: 1 and S0011: 1.		
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									S0142: 1, S0422: 1, L0770: 1, L0761: 1, L0771: 1, L0775: 1, L0653: 1, L0634: 1, L0659: 1, L0544: 1, L0664: 1, H0144: 1, S0126: 1, H0670: 1, H0555: 1, H0436: 1, H0627: 1, S0028: 1, L0780: 1, L0731: 1, L0757: 1, L0361: 1, S0026: 1, S0412: 1 and L0697: 1.			
82	HSPAB58	736098	92	3 - 116	992	Ser-20 to Tyr-25.		AR089: 1, AR061: 0 H0478: 1, L0748: 1 and L0749: 1.				
83	HSQCM85	963554	93	184 - 444	993			AR050: 19, AR054: 9, AR051: 5, AR089: 1, AR061: 0 S0216: 1 and S0026: 1.				
84	HTOIA82	844319	94	41 - 286	994	Arg-44 to Gly-59.		AR061: 4, AR089: 2 H0264: 1 and L0754: 1.				
85	HUUDH57	931155	95	2 - 2167	995	Pro-52 to Thr-58, Pro-115 to Asp-122, Asp-190 to Ile-208.		AR089: 11, AR061: 1 H0543: 4, S0354: 3, H0423: 3, H0656: 2, L0749: 2, H0306: 1, H0638: 1, S0356: 1, S0358: 1, S0360: 1, H0637: 1 S0046: 1				

								S0132: 1, H0486: 1, H0090: 1, S0112: 1, T0042: 1, H0494: 1, S0210: 1, L0770: 1, L0662: 1, L0659: 1, L0665: 1, H0682: 1, L0779: 1, H0445: 1, H0653: 1 and S0424: 1.			
86	HWACV74	1145916	96	960 - 745	996			AR089: 2, AR061: 1 H0581: 2, H0657: 1, S0358: 1, S0046: 1, S0222: 1, H0486: 1, H0551: 1, L0761: 1, L0766: 1, L0774: 1, L0659: 1, L0666: 1, L0664: 1 and H0435: 1.			
87	HWAFW39	947915	97	188 - 370	997		Ser-26 to Ser-33.	AR089: 2, AR061: 1 H0255: 1 and H0581: 1.			
88	HWBBER65	1156447	98	2076 - 1705	998		Lys-1 to Gln-8, Gln-28 to Gly-34, Pro-46 to Arg-51.	AR089: 28, AR061: 24 L0748: 2, H0580: 1 and H0421: 1.			
89	HWME65	969190	99	2 - 382	999		Gly-1 to Ser-9. Asp-30 to Trp-35, Ser-38 to Arg-43.	AR089: 17, AR061: 11 S0358: 2 and H0539: 1.			
90	HISBG28	920850	100	184 - 816	1000		Leu-91 to Glu-98, Ile-110 to Tyr-116, Ser-160 to Thr-168, Gly-175 to His-182.	AR061: 0, AR089: 0 L0766: 10, L0779: 3, L0759: 2, S0114: 1, S0116: 1, H0431: 1,			

91	HAIAB60	786337	101	3 - 377	1001	Pro-32 to His-49.	H0013: 1, H0251: 1, H0628: 1, H0646: 1, L0761: 1, L0662: 1, L0776: 1, L0665: 1, H0702: 1, H0520: 1, H0539: 1, L0749: 1, L0750: 1, H0444: 1, H0445: 1 and H0543: 1. AR089: 1, AR061: 1 L0439: 13, L0740: 12, q13.31 H0046: 10, H0556: 9, L0752: 9, H0052: 7, H0617: 7, L0748: 7, L0758: 7, S0222: 6, L0754: 6, S0049: 5, H0620: 5, S0002: 5, L0769: 5, L0438: 5, L0741: 5, L0731: 5, S0278: 4, H0599: 4, S0010: 4, L0163: 4, L0804: 4, L0663: 4, H0144: 4, H0521: 4, L0742: 4, L0743: 4, L0751: 4, L0753: 4, H0657: 3, H0618: 3, H0050: 3, L0471: 3, S0051: 3, T0010: 3, S6028: 3, H0266: 3, H0551: 3, H0494: 3, S0144: 3, H0529: 3,	22q13.2- q13.31	188826, 250100, 250800, 250800	
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	L0763: 3, L0770: 3, L0771: 3, L0766: 3, L0775: 3, L0659: 3, L0809: 3, L0666: 3, S0330: 3, H0696: 3, L0747: 3, L0757: 3, L0759: 3, H0265: 2, H0656: 2, S0418: 2, L0149: 2, H0333: 2, H0427: 2, H0042: 2, H0590: 2, H0457: 2, H0041: 2, S0003: 2, T0006: 2, S0364: 2, H0124: 2, S0366: 2, H0135: 2, L0638: 2, L0637: 2, L0372: 2, L0662: 2, L0776: 2, L0655: 2, L0789: 2, S0374: 2, H0658: 2, H0660: 2, S0152: 2, L0485: 2, L0599: 2, L0601: 2, H0506: 2, S0040: 1, H0650: 1, H0341: 1, S0212: 1, S0282: 1, H0663: 1, H0459: 1, H0638: 1, S0420: 1, L0617: 1, S0360: 1, S0408: 1, H0208: 1, S0132: 1, H0645: 1, H0370: 1, L0622: 1, L0623: 1,	
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	H0486: 1, H0013: 1, S0280: 1, H0156: 1, L0021: 1, H0097: 1, H0575: 1, H0036: 1, S0346: 1, H0318: 1, H0230: 1, H0596: 1, H0597: 1, H0231: 1, H0150: 1, H0009: 1, N0006: 1, H0242: 1, H0012: 1, H0024: 1, H0373: 1, H0051: 1, H0083: 1, H0267: 1, H0292: 1, H0604: 1, H0553: 1, H0181: 1, H0168: 1, H0163: 1, H0090: 1, T0067: 1, H0264: 1, S0038: 1, S0386: 1, S0112: 1, L0351: 1, T0042: 1, H0561: 1, S0370: 1, S0142: 1, S0344: 1, L0640: 1, L0761: 1, L0667: 1, L0373: 1, L0646: 1, L0641: 1, L0374: 1, L0764: 1, L0773: 1, L0521: 1, L0626: 1, L0794: 1, L0533: 1, L0651: 1, L0376: 1, L0806: 1, L0805: 1, L0657: 1, L0634: 1, L0542: 1,	
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									L0783: 1, L0529: 1, L0787: 1, L0665: 1, H0519: 1, S0380: 1, H0522: 1, H0436: 1, H0576: 1, L0609: 1, L0744: 1, L0745: 1, L0749: 1, L0786: 1, L0777: 1, L0755: 1, H0444: 1, L0584: 1, L0595: 1, S0011: 1, H0422: 1 and H0008: 1.		
92	HDPDE32	1217181	102	39 - 890	1002	Arg-25 to Glu-30.			AR089: 10, AR061: 3 H0703: 7, H0494: 3, H0699: 3, H0542: 3, H0546: 1, H0684: 1, H0521: 1, S0031: 1 and H0543: 1.		
93	HBDAC79	973342 1199232	700 103	165 - 647 82 - 477	1600 1003	Asn-1 to Arg-6. Lys-12 to Lys-19, Phe-48 to Phe-57, Gly-120 to Gly-126.			AR089: 2, AR061: 1 H0556: 2, L0766: 2, S0418: 1, S0442: 1, H0393: 1, H0261: 1, S0222: 1, H0545: 1, H0050: 1, S6028: 1, H0551: 1, H0494: 1, S0144: 1, S0002: 1, H0529: 1, H0521: 1, L0439: 1, L0759: 1, S0308: 1, L0366: 1 and H0506: 1.		

94	HEMDX48	935414	701	1 - 366	1601	Met-4 to Lys-12, Phe-41 to Phe-50. Ala-32 to Thr-39, Glu-88 to Lys-107, Thr-165 to Tyr-172, Thr-204 to Lys-210, Thr-262 to Gly-271, Thr-335 to Leu-343, Arg-476 to Leu-482, Ser-504 to Cys-514, Gln-592 to Val-608, Pro-623 to Cys-628.	AR061: 7, AR089: 3 L0666: 4, L0747: 4, L0783: 3, L0665: 3, L0602: 3, S0222: 2, H0318: 2, H0553: 2, H0135: 2, L0763: 2, L0772: 2, L0662: 2, H0660: 2, H0436: 2, L0743: 2, L0751: 2, L0750: 2, L0411: 1, H0265: 1, H0556: 1, H0685: 1, S0418: 1, S0420: 1, S0358: 1, S0046: 1, L0717: 1, H0351: 1, S6014: 1, H0431: 1, H0486: 1, H0013: 1, H0253: 1, H0052: 1, L0157: 1, H0271: 1, H0617: 1, H0090: 1, H0494: 1, H0396: 1, H0509: 1, H0652: 1, S0002: 1, S0426: 1, L0769: 1, L0764: 1, L0767: 1, L0766: 1, L0775: 1, L0806: 1, L0809: 1, T0068: 1, H0693: 1, L0352: 1, H0520: 1,
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95	HHASB48	521844	702	1 - 321	1602	Thr-47 to Gly-56.	H0547: 1, S0152: 1, H0521: 1, S0404: 1, H0555: 1, S0027: 1, S0028: 1, L0779: 1, L0780: 1, L0752: 1, L0755: 1, L0731: 1, L0758: 1, H0707: 1, L0593: 1, L0603: 1, H0136: 1 and S0242: 1.		
		721150	105	46 - 651	1005	Ala-32 to Thr-39, Glu-88 to Lys-107, Thr-165 to Tyr-172.	AR061: 0, AR089: 0, L0666: 4, L0747: 4, L0783: 3, L0665: 3, L0602: 3, S0222: 2, H0318: 2, H0553: 2, H0135: 2, L0763: 2, L0772: 2, L0662: 2, H0660: 2, H0436: 2, L0743: 2, L0751: 2, L0750: 2, L0411: 1, H0265: 1, H0556: 1, H0685: 1, S0418: 1, S0420: 1, S0358: 1, S0046: 1, L0717: 1, H0351: 1, S6014: 1, H0431: 1, H0486: 1, H0013: 1, H0253: 1, H0052: 1, L0157: 1, H0271: 1, H0617: 1, H0090: 1, H0494: 1		

									H0396: 1, H0509: 1, H0652: 1, S0002: 1, S0426: 1, L0769: 1, L0764: 1, L0767: 1, L0766: 1, L0775: 1, L0806: 1, L0809: 1, T0068: 1, H0693: 1, L0352: 1, H0520: 1, H0547: 1, S0152: 1, H0521: 1, S0404: 1, H0555: 1, S0027: 1, S0028: 1, L0779: 1, L0780: 1, L0752: 1, L0755: 1, L0731: 1, L0758: 1, H0707: 1, L0593: 1, L0603: 1, H0136: 1 and S0242: 1.			
96	HLWCA17	1104762	106	326 - 1012	1006				AR089: 13, AR061: 4 S0358: 1, S0046: 1, H0592: 1, H0036: 1, H0318: 1, S0003: 1, H0553: 1, L0766: 1, H0672: 1, L0439: 1, L0756: 1, L0755: 1, L0731: 1 and L0757: 1.			
		957664	703	515 - 934	1603							
97	HNTTD09	1104487	107	152 - 940	1007				AR061: 1, AR089: 0 H0656: 1, H0587: 1, H0036: 1, H0590: 1, L0143: 1, H0547: 1			

98	HSKDT07	676665 927823	704 108	3 - 425 1 - 918	1604 1008	AR061: 7, AR089: 4 L0666: 4, L0747: 4, L0783: 3, L0665: 3, L0602: 3, S0222: 2, H0318: 2, H0553: 2, H0135: 2, L0763: 2, L0772: 2, L0662: 2, H0660: 2, H0436: 2, L0743: 2, L0751: 2, L0750: 2, L0411: 1, H0265: 1, H0556: 1, H0685: 1, S0418: 1, S0420: 1, S0358: 1, S0046: 1, L0717: 1, H0351: 1, S6014: 1, H0431: 1, H0486: 1, H0013: 1, H0253: 1, H0052: 1, L0157: 1, H0271: 1, H0617: 1, H0090: 1, H0494: 1, H0396: 1, H0509: 1, H0652: 1, S0002: 1, S0426: 1, L0769: 1, L0764: 1, L0767: 1, L0766: 1, L0775: 1, L0806: 1, L0809: 1, T0068: 1, H0693: 1, L0352: 1, H0520: 1	H0689: 1 and H0653: 1.		
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									H0547: 1, S0152: 1, H0521: 1, S0404: 1, H0555: 1, S0027: 1, S0028: 1, L0779: 1, L0780: 1, L0752: 1, L0755: 1, L0731: 1, L0758: 1, H0707: 1, L0593: 1, L0603: 1, H0136: 1 and S0242: 1.		
99	HSRDB26	1102231	109	21 - 410	1009				AR089: 1, AR061: 1 S0022: 1, S0028: 1 and S0260: 1.		
100	HAPBS07	525475 967325	705 110	15 - 347 1 - 315	1605 1010			Glu-44 to Pro-49.	AR061: 5, AR089: 2 S0002: 4, S0344: 3, S0278: 2, S0358: 1, H0042: 1, H0575: 1, S0010: 1, H0373: 1, S0003: 1, H0163: 1, H0038: 1, H0616: 1, H0264: 1, H0100: 1, S0144: 1 and H0521: 1.		
101	HAUAI17	921674	111	118 - 780	1011			Lys-50 to Gly-55, Thr-73 to Val-78, Thr-85 to Arg-91, Pro-103 to Ser-112, Leu-199 to Ser-207, Pro-209 to Ser-214.	AR061: 2, AR089: 1 L0803: 6, L0748: 5, L0749: 4, H0424: 3, L0804: 3, L0774: 3, L0779: 3, H0213: 2, S0142: 2, L0789: 2, L0745: 2, L0731: 2, H0294: 1, H0254: 1,		

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									S0360: 2, H0550: 2, S0028: 2, H0543: 2, H0663: 1, H0638: 1, S0376: 1, H0580: 1, S0045: 1, H0393: 1, H0370: 1, H0392: 1, H0156: 1, H0618: 1, H0318: 1, H0135: 1, T0042: 1, H0366: 1, S0002: 1, L0803: 1, L0791: 1, S0126: 1, S0037: 1, S0027: 1, S0032: 1, L0741: 1, L0754: 1, H0445: 1, L0596: 1, S0026: 1 and H0542: 1.			
104	HBGDA14	866258	114	3 - 503	1014	Gln-9 to Gln-16, Thr-33 to Gly-42, Gly-94 to Gln-101, Asp-108 to Arg-114.			AR061: 794, AR089: 295 S0050: 2, S0031: 2, S0260: 2, H0181: 1, H0617: 1 and S0390: 1.			
105	HCHNJ32	934848	115	3 - 764	1015	Thr-1 to Ser-9, Ser-146 to Thr-154, Thr-200 to Lys-208.			AR061: 113, AR089: 26 L0748: 15, L0581: 11, H0510: 9, H0617: 9, L0755: 7, H0484: 6, H0673: 6, L0769: 6, L0758: 5, S0278: 4, H0327: 4, H0124: 4, L0774: 4, L0526: 4,			

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106	HCHON59	931082	116	511 - 1344	1016	Gln-93 to Thr-99, Pro-124 to Gln-129.	AR089: 1, AR061: 0. L0748: 8, L0439: 6.	S0316: 1, H0687: 1, H0615: 1, H0428: 1, H0604: 1, H0181: 1, H0606: 1, H0032: 1, H0674: 1, S0036: 1, H0090: 1, H0038: 1, H0616: 1, H0087: 1, H0413: 1, H0129: 1, H0494: 1, S0144: 1, S0142: 1, S0344: 1, L0520: 1, L0763: 1, L0638: 1, L0772: 1, L0372: 1, L0768: 1, L0794: 1, L0766: 1, L0775: 1, L0607: 1, L0657: 1, L0783: 1, L0384: 1, L0809: 1, L0519: 1, L0543: 1, L0368: 1, S0052: 1, S0374: 1, H0689: 1, H0539: 1, S0378: 1, H0521: 1, H0694: 1, S0188: 1, H0134: 1, S3014: 1, S0027: 1, L0744: 1, L0745: 1, L0752: 1, H0595: 1, L0605: 1, L0604: 1, H0136: 1 and H0543: 1.		
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107	HCUGN19	716989	117	35 - 382	1017	Glu-58 to Gly-64, Pro-77 to Cys-93, Pro-96 to Pro-106.	Glu-153 to Leu-159, Gln-162 to Gly-168, Ser-198 to Gly-203, Lys-210 to Asn-215, Gly-219 to Gln-224.	L0766: 4, L0803: 4, L0749: 3, S0358: 2, H0574: 2, H0327: 2, H0539: 2, L0758: 2, S0026: 2, S0212: 1, H0484: 1, S0354: 1, S0046: 1, H0592: 1, T0114: 1, H0427: 1, H0590: 1, H0581: 1, H0046: 1, H0081: 1, H0015: 1, H0051: 1, T0006: 1, H0040: 1, H0268: 1, S0438: 1, S0422: 1, H0529: 1, L0763: 1, L0770: 1, L0662: 1, L0794: 1, L0649: 1, L0775: 1, L0515: 1, L0792: 1, H0520: 1, H0547: 1, H0435: 1, S0328: 1, S0380: 1, S0152: 1, H0521: 1, L0356: 1, L0747: 1, L0753: 1, L0485: 1 and H0423: 1.		
108	HCUGR38	706471	118	3 - 317	1018	Ser-2 to His-7, Pro-14 to Leu-20, Ala-33 to Gly-38	Glu-58 to Gly-64, Pro-77 to Cys-93, Pro-96 to Pro-106.	AR089: 7, AR061: 2 L0744: 3, L0766: 2, H0402: 1 and L0754: 1.		

109	HDPND85	852628	119	68 - 853	1019	Ser-1 to Pro-10.	AR089: 0, AR061: 0 L0747: 6, H0638: 3, L0758: 3, L0157: 2, H0529: 2, L0764: 2, L0774: 2, L0776: 2, H0521: 2, H0522: 2, L0779: 2, L0603: 2, H0662: 1, S0358: 1, S0222: 1, H0038: 1, H0625: 1, S0448: 1, L0371: 1, L0770: 1, L0796: 1, L0775: 1, L0809: 1, L0791: 1, L0666: 1, H0144: 1, H0520: 1, H0436: 1, L0748: 1, L0755: 1 and L0731: 1.		
110	HDPN38	883658	120	78 - 749	1020	Leu-60 to Gln-65, Arg-76 to Val-81.	AR089: 11, AR061: 3 H0510: 2, L0666: 2, L0740: 2, L0595: 2, H0657: 1, H0580: 1, H0619: 1, H0357: 1, H0632: 1, H0013: 1, H0024: 1, H0578: 1, H0591: 1, H0509: 1, L0769: 1, L0804: 1, L0774: 1, L0805: 1, L0776: 1, L0527: 1, H0521: 1, H0555: 1, L0749: 1, L0757: 1 and		

111	HE8AM92	952610	121	157 - 603	1021	Met-9 to Glu-16, Glu-41 to Trp-47, Arg-55 to Glu-62, Asp-135 to Pro-149.	H0423: 1, AR061: 28, AR089: 11 L0439: 21, L0438: 13, H0144: 6, H0521: 6, H0543: 5, H0013: 4, S0003: 4, L0740: 4, L0766: 3, L0759: 3, L0588: 3, S0116: 2, H0662: 2, S0358: 2, L0738: 2, H0046: 2, S0214: 2, H0039: 2, H0591: 2, H0264: 2, H0560: 2, L0770: 2, L0764: 2, L0803: 2, L0774: 2, L0659: 2, L0666: 2, H0670: 2, H0672: 2, L0743: 2, L0749: 2, L0752: 2, L0731: 2, L0758: 2, H0445: 2, H0170: 1, H0265: 1, H0583: 1, H0657: 1, S0282: 1, S0376: 1, S0360: 1, H0580: 1, H0261: 1, S0222: 1, H0586: 1, H0497: 1, L0021: 1, H0575: 1, H0036: 1, H0318: 1, H0581: 1, H0251: 1, T0115: 1, L0040: 1, H0327: 1,		
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112	HE9RE21	888243	122	3 - 422	1022	Arg-3 to Ser-15, Ser-103 to Gln-111.	S0388: 1, T0010: 1, H0266: 1, H0687: 1, S0250: 1, S0022: 1, H0622: 1, S0036: 1, H0090: 1, H0040: 1, T0067: 1, H0488: 1, H0413: 1, H0494: 1, S0150: 1, H0641: 1, S0002: 1, L0598: 1, H0529: 1, L0374: 1, L0771: 1, L0773: 1, L0521: 1, L0794: 1, L0775: 1, L0655: 1, L0606: 1, L0657: 1, L0663: 1, S0374: 1, H0520: 1, S0126: 1, H0659: 1, S0152: 1, S0432: 1, S0028: 1, L0750: 1, L0779: 1, L0777: 1, H0707: 1, L0589: 1, L0599: 1, L0593: 1, H0136: 1, S0242: 1, H0423: 1 and H0422: 1.		
							AR089: 10, AR061: 3 H0556: 1, S0114: 1, S0134: 1, S0360: 1, T0082: 1, H0052: 1, H0644: 1, H0551: 1, L0770: 1, L0789: 1.		

									H0144: 1, H0435: 1 and H0436: 1.			
113	HETKH30	884009	123	90 - 884	1023	Arg-1 to Lys-8.			AR061: 1, AR089: 1 H0046: 5, H0040: 2, H0519: 2, L0439: 2, L0758: 2, H0575: 1 and T0042: 1.			
114	HHAME78	840939	124	3 - 263	1024				AR089: 1, AR061: 1 H0624: 1, S0420: 1, S0366: 1, H0135: 1, H0494: 1, S0422: 1, L0745: 1 and L0758: 1.			
115	HKABI68	856590	125	1 - 471	1025	Arg-20 to Arg-30, Arg-74 to Lys-82.			AR089: 23, AR061: 12 S0046: 1, H0100: 1, H0494: 1, H0521: 1, H0522: 1 and S0028: 1.			
116	HKMLN95	914083	126	2 - 583	1026				AR089: 7, AR061: 2 S0003: 5, S0354: 2, S0214: 2, H0519: 2, H0689: 2, H0522: 2, L0748: 2, L0439: 2, L0731: 2, L0759: 2, H0171: 1, T0002: 1, S0040: 1, H0669: 1, S0356: 1, S0360: 1, H0431: 1, H0586: 1, H0574: 1, H0632: 1, H0156: 1, H0590: 1, T0110: 1, L0471: 1, S6028: 1, H0628: 1,			

									S0036: 1, H0494: 1, S0450: 1, S0144: 1, L0803: 1, L0438: 1, H0520: 1, H0547: 1, H0660: 1, S0328: 1, H0521: 1, S0434: 1, L0605: 1, L0599: 1, L0593: 1 and H0543: 1.			
117	HMCFA91	959954	127	1 - 729	1027	Cys-1 to Ala-10.			AR061: 87, AR089: 61 L0803: 6, L0766: 3, L0758: 3, L0790: 2, L0743: 2, L0748: 2, L0747: 2, L0750: 2, L0779: 2, L0755: 2, H0255: 1, H0370: 1, H0530: 1, H0150: 1, S0344: 1, L0763: 1, L0769: 1, L0637: 1, L0764: 1, L0804: 1, L0774: 1, L0805: 1, L0776: 1, L0783: 1, L0809: 1, L0664: 1, L0665: 1, L0752: 1, L0731: 1, L0681: 1 and H0543: 1.			
118	HNTBF75	836701	128	43 - 330	1028				AR089: 13, AR061: 5 S0003: 5, S0354: 2, S0214: 2, H0519: 2, H0689: 2, H0522: 2, L0748: 2, L0439: 2,			

									L0731: 2, L0759: 2, H0171: 1, T0002: 1, S0040: 1, H0669: 1, S0356: 1, S0358: 1, S0360: 1, H0431: 1, H0586: 1, H0574: 1, H0632: 1, H0156: 1, H0575: 1, H0590: 1, T0110: 1, L0471: 1, S6028: 1, H0628: 1, S0036: 1, H0494: 1, S0450: 1, S0144: 1, L0803: 1, L0809: 1, L0438: 1, H0520: 1, H0547: 1, H0660: 1, S0328: 1, H0521: 1, S0434: 1, L0605: 1, L0599: 1, L0593: 1, H0668: 1 and H0543: 1.			
119	HPTGB43	726460	129	3 - 266	1029	His-1 to Ser-8, Thr-68 to Lys-76.			AR089: 9, AR061: 7			
120	HPTVL90	509487	130	2 - 211	1030	Pro-48 to Ile-54.			AR061: 1, AR089: 0 L0803: 6, L0748: 5, L0749: 4, H0424: 3, L0804: 3, L0774: 3, L0779: 3, H0213: 2, S0142: 2, L0789: 2, L0745: 2, L0731: 2, H0294: 1, H0254: 1, H0393: 1 H0549: 1			

121	HSKIA89	837986	131	296 - 634	1031							H0427: 1, H0156: 1, T0082: 1, H0052: 1, H0150: 1, H0024: 1, H0135: 1, H0268: 1, H0100: 1, S0344: 1, L0763: 1, L0769: 1, L0662: 1, L0775: 1, L0805: 1, L0657: 1, L0666: 1, H0144: 1, L0740: 1, L0750: 1 and L0755: 1.		
122	HTXGF27	695766	132	1 - 1011	1032	Gly-1 to Gly-6, Ser-16 to Ala-23, Thr-114 to Lys-120, Thr-274 to Ser-280, Arg-327 to Ser-337.						AR089: 8, AR061: 2 L0471: 1, S0150: 1, H0435: 1, H0539: 1 and S3014: 1. AR061: 3, AR089: 3 L0769: 5, L0752: 5, S0358: 4, H0448: 4, L0754: 4, H0052: 3, L0773: 3, L0666: 3, L0740: 3, L0750: 3, L0596: 3, H0370: 2, H0024: 2, H0083: 2, H0031: 2, H0090: 2, S0142: 2, L0766: 2, L0663: 2, L0747: 2, L0753: 2, L0588: 2, L0599: 2, H0265: 1, S0040: 1, H0583: 1, H0656: 1 S0442: 1		

123	HWHHW54	684125	133	853 - 1146	1033	Pro-50 to Gly-69, Pro-71 to Lys-80.	H0393: 1, H0431: 1, L0622: 1, H0635: 1, S0280: 1, L0021: 1, H0002: 1, H0036: 1, H0421: 1, H0204: 1, H0046: 1, H0014: 1, H0015: 1, S6028: 1, H0266: 1, H0169: 1, S0366: 1, H0040: 1, H0264: 1, S0038: 1, H0494: 1, L0772: 1, L0372: 1, L0374: 1, L0644: 1, L0765: 1, L0771: 1, L0364: 1, L0806: 1, L0659: 1, L0783: 1, L0647: 1, L0665: 1, H0435: 1, H0658: 1, H0214: 1, L0751: 1, L0731: 1, L0758: 1, L0759: 1, H0653: 1, L0462: 1 and H0352: 1.		
124	HWHPO29	857383	134	236 - 670	1034		AR089: 3, AR061: 1 L0748: 6, L0747: 2, H0170: 1, H0586: 1, S0051: 1, H0163: 1, L0665: 1, H0670: 1, H0660: 1 and H0423: 1.		

125	HWLPR94	967326	135	184 - 459.	1035	Thr-29 to Gly-34, Glu-53 to Leu-58, Thr-66 to Thr-74.	L0439: 2, H0592: 1, H0587: 1, L0021: 1, L0456: 1, H0494: 1, S0448: 1, L0662: 1 and L0774: 1. AR089: 18, AR061: 3 L0766: 4, L0666: 3, S0278: 2, L0758: 2, S0358: 1, S0376: 1, S0010: 1, H0050: 1, S0003: 1, H0038: 1, H0616: 1, H0264: 1, H0100: 1, S0448: 1, S0344: 1, S0002: 1, S0426: 1, L0642: 1, L0659: 1, S0374: 1, H0521: 1 and : 1.				
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126	HWLUL28	925331	136	1 - 750	1036	Arg-11 to Pro-19, Pro-36 to Asp-44, Lys-183 to Gly-189, Thr-201 to Arg-207.	AR089: 16, AR061: 9 L0439: 3, S0360: 2, H0615: 2, L0770: 2, L0666: 2, L0438: 2, L0749: 2, L0758: 2, L0596: 2, H0294: 1, H0351: 1, S0222: 1, H0441: 1, H0611: 1, H0599: 1, H0251: 1, H0046: 1, H0567: 1, H0081: 1, H0083: 1, H0213: 1, H0617: 1, L0055: 1, H0494: 1, H0560: 1, L0769: 1, L0761: 1, L0766: 1, L0649: 1, L0774: 1, L0775: 1, L0375: 1, L0805: 1, L0657: 1, L0526: 1, L0789: 1, L0665: 1, H0519: 1, H0658: 1, S0380: 1, L0748: 1, L0786: 1, L0777: 1, L0731: 1 and H0543: 1.	16p13.3	141750, 141800, 141800, 141800, 141800, 141850, 141850, 141850, 141850, 156850, 186580, 191092, 600140, 600273, 601313, 601785
127	HWLXT48	957630	137	55 - 363	1037		AR089: 12, AR061: 9 S0360: 2, H0550: 2, S0028: 2, H0543: 2, H0663: 1, H0638: 1, S0376: 1, H0580: 1, S0045: 1, H0393: 1,		

128	HBGMD15	1103922	138	1 - 567	1038	Gly-1 to Ser-6.	H0370: 1, H0392: 1, H0156: 1, H0618: 1, H0318: 1, H0135: 1, T0042: 1, H0366: 1, S0002: 1, L0803: 1, L0791: 1, S0126: 1, S0037: 1, S0027: 1, S0032: 1, L0741: 1, L0754: 1, H0445: 1, L0596: 1, S0026: 1 and H0542: 1.		
129	HNGMA91	786307 789744	706 139	3 - 323 7 - 327	1606 1039	His-53 to Arg-61. His-8 to Gly-18.	AR089: 0, AR061: 0 H0617: 4 and S0028: 1. AR089: 1, AR061: 0		
130	HSLEI57	1103672 730927	140 707	2 - 640 2 - 433	1040 1607	 Gly-23 to Gly-28, Arg-73 to Asn-78.	AR089: 1, AR061: 0 S0044: 1 and S0028: 1.		
131	HSLFE21	1103524	141	2 - 1012	1041	Pro-52 to Ala-57, Tyr-110 to Lys-122.	AR061: 1, AR089: 1 H0246: 4, S0028: 3, H0197: 2, S0282: 1, H0199: 1 and S3020: 1.		
132	HSLIE40	823083 1105422	708 142	122 - 658 510 - 1	1608 1042	 	AR061: 5, AR089: 2 H0294: 1, S0044: 1 and S0028: 1.		
133	HTXHA35	866274 1152110	709 143	65 - 283 291 - 839	1609 1043	His-49 to Lys-54. Gln-130 to Asp-135,	AR061: 6, AR089: 3		

								H0124: 2, H0135: 2, H0265: 1, S0134: 1, H0657: 1, S0280: 1, H0122: 1, H0618: 1, H0251: 1, H0090: 1, H0646: 1, H0144: 1, L0743: 1 and L0748: 1.		
134	HAICS07	633682 1105538	710 144	247 - 501 157 - 810	1610 1044	Gly-75 to Cys-83.	Asp-167 to Leu-178.	AR089: 6, AR061: 6 S0132: 1, H0038: 1 and L0439: 1.		
		953351	711	157 - 810	1611	Met-104 to His-110, Arg-202 to Pro-214.				
135	HBKDN33	1167313	145	2 - 1015	1045	Ser-28 to Pro-34, Pro-134 to Ser-139, Gln-178 to Gly-183, Thr-193 to Gly-198, His-244 to Gly-257, Asp-263 to Tyr-273.		AR089: 1, AR061: 0 L0439: 2, H0506: 2, S0354: 1, S0358: 1, S0280: 1, H0622: 1, S0366: 1, H0059: 1, S0344: 1, H0658: 1, H0539: 1, H0521: 1, H0522: 1, H0555: 1, L0748: 1, L0751: 1, L0753: 1 and L0596: 1.		
		922414	712	2 - 1237	1612	Ser-28 to Pro-34, Pro-134 to Ser-139, Gln-178 to Gly-183, Thr-193 to Gly-198, His-244 to Gly-257, Asp-263 to Tyr-273, Lys-337 to Arg-347,				

136	HBODH62	1228278	146	293 - 1729	1046	Pro-366 to Lys-372, Ala-382 to Asp-387. Gln-10 to Gly-15, Lys-193 to Ser-199, Asp-323 to Tyr-332, Leu-425 to Gly-431, Lys-470 to Ala-477.	AR089: 0, AR061: 0 H0046: 5, L0769: 5, L0755: 4, L0758: 4, H0581: 3, L0803: 3, L0774: 3, L0600: 3, L0427: 2, S0358: 2, H0253: 2, H0252: 2, H0553: 2, H0087: 2, S0038: 2, L0517: 2, L0438: 2, L0748: 2, L0756: 2, L0777: 2, H0170: 1, H0265: 1, H0650: 1, H0657: 1, S0116: 1, S0442: 1, S0354: 1, H0370: 1, H0486: 1, H0013: 1, H0349: 1, H0706: 1, H0618: 1, H0327: 1, H0373: 1, H0428: 1, S0364: 1, H0124: 1, H0100: 1, L0770: 1, L0637: 1, L0761: 1, L0372: 1, L0800: 1, L0641: 1, L0768: 1, L0794: 1, L0766: 1, L0657: 1, L0635: 1, L0542: 1, L0809: 1, L0789: 1, L0666: 1,		
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137	HCEPJ44	742827 1157810	713 147	3 - 290 2 - 571	1613 1047	Gln-1 to Asp-8, Lys-142 to Asp-160.	L0665: 1, H0144: 1, H0682: 1, H0651: 1, S0380: 1, H0555: 1, L0439: 1, L0750: 1, L0780: 1, L0759: 1, L0366: 1, H0543: 1 and H0506: 1.		
138	HCWCM65	930790 1105668	714 148	3 - 536 3 - 659	1614 1048	Lys-130 to Asp-148. Ser-44 to His-57.	AR089: 6, AR061: 4 S0420: 1, H0052: 1, H0024: 1, H0649: 1, H0689: 1 and H0435: 1.		
139	HDQDY52	529230 1182322	715 149	1 - 360 43 - 597	1615 1049	Ser-45 to His-58. His-68 to Gly-73, Glu-81 to Glu-87.	AR089: 25, AR061: 24 H0521: 2, H0580: 1, H0393: 1, H0052: 1, H0081: 1, L0774: 1 and S0152: 1.		
140	HHEAA32	852622 1203140	716 150	43 - 597 499 - 1236	1616 1050	His-68 to Gly-73, Glu-81 to Glu-87. Arg-19 to Gln-28, Glu-35 to Ser-40, Gly-60 to Tyr-66.	AR061: 9, AR054: 6, AR089: 3, AR050: 1, AR051: 1 H0574: 2, H0510: 2, H0549: 1, H0331: 1, S0010: 1 and L0775: 1.		

[illegible]

Lys-378 to Ser-384.	L0755: 4, L0758: 4, H0581: 3, L0803: 3, L0774: 3, L0600: 3, L0427: 2, S0358: 2, H0253: 2, H0252: 2, H0553: 2, H0087: 2, S0038: 2, L0517: 2, L0438: 2, L0748: 2, L0756: 2, L0777: 2, H0170: 1, H0265: 1, H0650: 1, H0657: 1, S0116: 1, S0442: 1, S0354: 1, H0370: 1, H0486: 1, H0013: 1, H0349: 1, H0706: 1, H0618: 1, H0327: 1, H0373: 1, H0428: 1, S0364: 1, H0124: 1, H0100: 1, L0770: 1, L0637: 1, L0761: 1, L0372: 1, L0800: 1, L0641: 1, L0768: 1, L0794: 1, L0766: 1, L0657: 1, L0635: 1, L0542: 1, L0809: 1, L0789: 1, L0666: 1, L0665: 1, H0144: 1, H0682: 1, H0651: 1, S0380: 1, H0555: 1, L0439: 1, L0750: 1, L0780: 1, L0759: 1,
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								L0366: 1, H0543: 1 and H0506: 1.		
145	HLDPC46	574897	720	1 - 465	1620			Leu-1 to Glu-6, Arg-10 to Gln-19.	AR061: 2, AR089: 1 H0574: 2, H0510: 2, H0549: 1, H0331: 1, S0010: 1 and L0775: 1.	
		466567	155	2 - 595	1055					
146	HLDRG44	1106225	156	1 - 1026	1056			Gln-1 to Cys-12.	AR061: 13, AR089: 0 L0803: 10, L0774: 9, L0775: 6, L0651: 4, L0581: 4, H0510: 2, H0632: 1, H0156: 1, L0021: 1, H0015: 1, H0388: 1, H0509: 1, L0375: 1, L0790: 1, L0748: 1 and L0749: 1.	
		969544	721	2 - 946	1621			Asp-60 to Lys-65.		
147	HLICR73	1107517	157	3 - 539	1057			Asp-49 to Gly-55, Pro-73 to Thr-80, Thr-98 to Phe-103.	AR061: 9, AR089: 2 H0510: 3, L0393: 1, H0355: 1 and L0581: 1.	
		837030	722	1 - 444	1622			Asp-41 to Gly-47, Pro-65 to Thr-72, Thr-90 to Phe-95.		
148	HNHOP64	1103943	158	524 - 3	1058			Pro-51 to Phe-58.	AR089: 22, AR061: 7 H0483: 1, H0052: 1, H0553: 1 and S0216: 1.	
		966754	723	365 - 889	1623					
149	HSDEF56	1128288	159	1 - 744	1059				AR061: 0, AR089: 0 H0171: 1, T0042: 1 and S0031: 1.	

150	HTENI29	496551	724	2 - 490	1624	Pro-74 to Lys-84, Gln-107 to Trp-113.	AR061: 5, AR089: 3 L0748: 6, L0749: 6, L0758: 6, L0439: 5, L0794: 4, L0805: 3, L0438: 3, S0116: 2, H0574: 1, N0006: 1, H0616: 1, L0515: 1, L0809: 1, L0756: 1 and L0753: 1.		
151	HWMKD72	954519	725	3 - 1172	1625	Asp-1 to Arg-7.	AR089: 2, AR061: 1 L0803: 12, S0358: 2, L0748: 2, H0643: 1, H0494: 1, L0065: 1, L0800: 1, L0774: 1, L0657: 1, S0152: 1 and L0755: 1.		
152	HAPSQ21	970613	726	2 - 652	1626	Thr-95 to Gly-106, Pro-188 to Ser-193.	AR061: 2, AR089: 2 H0575: 6, H0042: 2, H0024: 2, L0774: 2, L0750: 2, L0599: 2, H0549: 1, H0375: 1, H0647: 1, H0646: 1, L0806: 1, L0791: 1 and L0779: 1.		
153	HLJDW02	1192885	163	617 - 3	1063	Arg-57 to Gln-76,	AR061: 2, AR089: 1		

154	HMGBT01	837592	1205666	727	2 - 517	1627	1064	<p>Glu-86 to Cys-98, Pro-112 to Cys-122, Ser-132 to Gly-143.</p> <p>Asp-1 to Gln-9, Leu-45 to Lys-62, Thr-69 to Glu-74, Pro-189 to Trp-194, Ile-205 to Leu-210, Tyr-217 to Ser-222, Ser-249 to Asp-256, Thr-311 to Tyr-317, Arg-344 to Ile-349.</p>	<p>H0549: 1, H0575: 1, H0375: 1, H0647: 1, L0774: 1 and L0779: 1.</p> <p>AR050: 12, AR054: 10, AR051: 2, AR089: 2, AR061: 0 L0439: 23, L0748: 18, L0438: 17, L0749: 10, L0794: 7, L0805: 6, L0740: 6, L0777: 6, H0013: 5, H0052: 5, L0770: 5, L0731: 5, L0803: 4, L0754: 4, L0750: 4, L0779: 4, L0752: 4, S0040: 3, H0551: 3, H0494: 3, H0538: 3, L0776: 3, L0809: 3, S0126: 3, S0378: 3, L0742: 3, L0747: 3, L0755: 3, S0222: 2, S0010: 2, H0327: 2, H0545: 2, H0266: 2, L0351: 2, L0800: 2, L0768: 2, L0774: 2, L0806: 2, L0665: 2, S0028: 2, L0744: 2, L0745: 2, L0756: 2, L0753: 2, L0757: 2, L0758: 2,</p>		
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155	HSSJJ24	879904 1178041	728 165	3 - 395 2 - 1171	1628 1065	Leu-6 to Gln-12, Leu-48 to Lys-65, Thr-72 to Glu-77, Pro-192 to Trp-197, Ile-208 to Leu-213, Tyr-220 to Ser-225, Ser-252 to Asp-259, Thr-314 to Tyr-320, Arg-347 to Ile-352.	AR061: 4, AR089: 0 L0439: 23, L0748: 18, L0438: 17, L0749: 10, L0794: 7, L0805: 6, L0740: 6, L0777: 6, H0013: 5, H0052: 5, L0770: 5, L0731: 5, L0803: 4, L0754: 4, L0750: 4, L0779: 4, L0752: 4, S0040: 3, H0551: 3, H0494: 3, H0538: 3, L0776: 3, L0809: 3, S0126: 3, S0378: 3, L0742: 3, L0747: 3, L0755: 3, S0222: 2, S0010: 2, H0327: 2, H0545: 2, H0266: 2, L0351: 2, L0800: 2, L0768: 2, L0774: 2, L0806: 2, L0665: 2, S0028: 2, L0744: 2, L0745: 2, L0756: 2, L0753: 2, L0757: 2, L0758: 2, L0759: 2, S0031: 2, S0260: 2, L0592: 2, H0171: 1, S6024: 1, H0650: 1, H0381: 1	H0352: 1.		
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101

157	HNTMD81	929511	167	1 - 492	1067	Ala-8 to Gly-14, His-44 to Ser-50, Tyr-70 to Thr-75, Ser-98 to Pro-113, Arg-119 to Phe-124, Ser-137 to Glu-154.	AR089: 5, AR061: 3 L0809: 1 and H0520: 1.	L0777: 2, H0123: 1 and L0747: 1.	302350, 306400, 309470, 309585, 311250, 312040, 312610, 314850
									104770, 107670, 110700, 135940, 145001, 146790, 152445, 152445, 159001, 174000, 179755, 182860, 182860, 182860, 191315, 230800, 230800, 266200, 600897, 601105, 601412, 601652.

158	HBSAJ60	1174334	168	2 - 1075	1068	Gly-24 to Lys-36.	AR089: 1, AR061: 1 S0028: 5, S0050: 3, L0591: 3, H0381: 2, H0623: 2, S0031: 2, S6024: 1, H0255: 1, H0305: 1, S0045: 1, S0278: 1, H0013: 1, S0280: 1, L0105: 1, H0271: 1, H0687: 1, H0634: 1, S0142: 1, S0126: 1, S0152: 1 and S0027: 1.		602491
159	HSKCI43	573965 506599	730 169	2 - 265 1 - 348	1630 1069	Ala-6 to Tyr-11, Gly-21 to Lys-33, Pro-54 to Trp-61, Ala-69 to Ile-75.	AR089: 2, AR061: 1 S0028: 5, S0050: 3, L0591: 3, H0381: 2, H0623: 2, S0031: 2, S6024: 1, H0255: 1, H0305: 1, S0045: 1, S0278: 1, H0013: 1, S0280: 1, L0105: 1, H0271: 1, H0687: 1, H0634: 1, S0142: 1, S0126: 1, S0152: 1 and S0027: 1.		
160	HSDKE47	1128095 764970	170 731	353 - 3 1 - 297	1070 1631	Asn-42 to Gly-47, Lys-55 to Ala-62.	AR089: 15, AR061: 6 S0260: 1 and L0581: 1.		

161	HCWTB56	1172460	171	400 - 2	1071	Leu-4 to Pro-10, Ser-15 to Ser-20.	AR061: 5, AR089: 4 H0305: 2 and H0589: 1.		
		853009	732	2 - 346	1632				
162	HFPBS73	1144027	172	370 - 1149	1072	Ala-72 to Asn-79, Asp-206 to Gly-211.	AR061: 7, AR089: 2 S0045: 2, S0028: 2, S0046: 1, S0222: 1, L0477: 1, H0042: 1, S3012: 1 and S0031: 1.		
		954892	733	3 - 590	1633	Ala-64 to Asn-71.			
163	HOEDD44	954893	173	44 - 583	1073		AR061: 1, AR089: 1 H0254: 2, H0255: 1, H0617: 1 and S0126: 1.		
164	HSUAN33	956315	174	1617 - 190	1074	Pro-28 to Lys-33, Pro-111 to Gln-116, Phe-161 to Ser-167, Pro-289 to Phe-301, Ser-305 to Asp-314.	AR061: 982, AR089: 580 L0527: 2, H0208: 1, H0635: 1, S0250: 1, H0622: 1, H0551: 1, L0766: 1, H0519: 1, H0521: 1, S0027: 1 and H0136: 1.		
165	HBCMD49	1206021	175	1 - 366	1075	Glu-47 to Thr-52.	AR061: 1, AR089: 0 L0774: 3, H0068: 2, L0622: 1, H0119: 1, H0509: 1, L0775: 1, L0776: 1, L0666: 1, S0028: 1, L0758: 1, S0260: 1 and S0396: 1.		
		865314	734	2 - 619	1634	Arg-1 to Leu-6, Pro-47 to Arg-52.			

166	HKABN12	956826	176	900 - 478	1076		AR089: 12, AR061: 6		
167	HMOAC31	1228291	177	1156 - 2640	1077	His-40 to Asn-46, Ser-101 to Lys-107, Ile-179 to Arg-184, Trp-223 to Cys-230, Phe-300 to Phe-306, Lys-353 to Gly-360, Leu-477 to Arg-490.	AR089: 1, AR061: 1 H0624: 2, S0001: 2, L0005: 1, S0045: 1, H0619: 1, H0191: 1, L0105: 1, H0165: 1, S0144: 1, S0428: 1 and S0031: 1.		
		920386	735	2 - 523	1635				
168	HMVBO92	1204710	178	1686 - 2108	1078	Gly-21 to Pro-27, Gln-62 to Asp-67, Asn-117 to Leu-124, Arg-131 to Phe-138.	AR089: 22, AR061: 9 L0748: 13, H0457: 9, L0751: 7, L0665: 6, L0766: 5, L0758: 5, S0358: 4, L0774: 4, H0144: 4, L0749: 4, L0777: 4, H0014: 3, L0662: 3, L0775: 3, L0776: 3, L0743: 3, L0747: 3, L0581: 3, L0600: 3, H0052: 2, L0640: 2, L0659: 2, L0526: 2, L0809: 2, S0126: 2, H0696: 2, L0439: 2, L0746: 2, L0750: 2, L0753: 2, H0295: 1, S0134: 1, S0212: 1, S0376: 1, S0045: 1, H0619: 1, H0261: 1, H0550: 1,		

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	L0747: 3, L0581: 3, L0600: 3, H0052: 2, L0640: 2, L0659: 2, L0526: 2, L0809: 2, S0126: 2, H0696: 2, L0439: 2, L0746: 2, L0750: 2, L0753: 2, H0295: 1, S0134: 1, S0212: 1, S0376: 1, S0045: 1, H0619: 1, H0261: 1, H0550: 1, H0333: 1, H0331: 1, H0486: 1, H0427: 1, H0575: 1, H0085: 1, H0204: 1, H0046: 1, H0012: 1, H0057: 1, S0051: 1, H0510: 1, H0188: 1, H0687: 1, H0169: 1, H0090: 1, H0591: 1, T0067: 1, H0488: 1, L0374: 1, L0648: 1, L0551: 1, L0376: 1, L0807: 1, L0790: 1, L0791: 1, L0666: 1, H0547: 1, H0519: 1, H0660: 1, H0672: 1, H0539: 1, H0555: 1, H0436: 1, S0028: 1, L0752: 1, L0755: 1, L0759: 1 and S0192: 1.
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170	HSSGE35	863712	737	1440 - 1943	1637	Ser-1 to Arg-13, Glu-32 to Ser-39.	AR089: 15, AR061: 13 T0006: 1 and H0135: 1.			
		1228152	180	1 - 516	1080	His-5 to Thr-13, Leu-26 to Ser-33, Gln-93 to Asp-98, Asn-148 to Leu-155, Arg-162 to Phe-169.				
		967832	738	1 - 396	1638	Ser-3 to Ser-11.				
171	HEMFJ74	1216651	181	52 - 1368	1081	Glu-11 to Ala-41, Pro-59 to Glu-64, Gly-90 to Arg-98, Glu-115 to Ser-121, Ser-150 to Gly-158, Phe-186 to Thr-192, Asp-204 to Glu-209, Ser-256 to Ser-261, Thr-283 to Asp-289, Val-341 to Ala-352, Asp-405 to Trp-422.	AR089: 16, AR061: 2 H0519: 2, S0040: 1, S0046: 1, H0455: 1, H0427: 1, H0599: 1, H0052: 1, H0038: 1, H0551: 1, H0269: 1, S0126: 1, H0689: 1, H0539: 1 and L0750: 1.			
		523350	739	1 - 348	1639	Gly-1 to Cys-39.				
172	HISCL24	676997	182	3 - 452	1082	Phe-10 to Thr-16, Asp-28 to Glu-33.	AR089: 0, AR061: 0 H0519: 2, S0040: 1, S0046: 1, H0455: 1, H0427: 1, H0599: 1, H0052: 1, H0038: 1, H0551: 1, H0269: 1, S0126: 1, H0689: 1, H0539: 1 and L0750: 1.	5q34-q35	109690, 109690, 123101, 164040, 180071, 208100, 246530, 600584	
173	H7PBB83	1228150	183	1 - 1110	1083		AR061: 1, AR089: 0 S0252: 5, S0268: 5,			

									S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, L0717: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0445: 2, H0657: 1, S0212: 1, H0580: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0266: 1, H0412: 1, L0637: 1, L0766: 1, S0053: 1, S0380: 1, L0755: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1, H0543: 1 and H0423: 1.			
174	HAGBA63	908235 1122199	740 184	756 - 301 1121 - 66	1640 1084	Glu-87 to Thr-94. Ser-13 to Leu-22, Phe-40 to Lys-45.	AR061: 4, AR089: 2 L0742: 3, S0010: 2, H0650: 1, S6026: 1, H0068: 1, L0794: 1 and L0809: 1.					
		509775	741	2 - 361	1641	Ser-13 to Leu-22, Phe-40 to Lys-45.						
175	HBMUG47	1102698	185	3 - 551	1085	Arg-1 to Lys-9.	AR089: 11, AR061: 11 L0665: 3, S0116: 1 and H0597: 1.					
		863846 1130816	742 186	1 - 315 3 - 1676	1642 1086	Gln-59 to Ser-71. Ser-8 to Gln-14, Asp-52 to Pro-63,	AR061: 2, AR089: 1 H0662: 2, S0003: 2,					
176	HCRFZ84											

177	HCWTR54	1192287	187	39 - 311	1087	Lys-172 to Lys-183, Thr-204 to Glu-210, Thr-227 to Ile-239, Ala-251 to Lys-258, Pro-276 to Glu-286, Glu-293 to Glu-304, Asn-338 to Lys-343, Asp-350 to Lys-372, Leu-374 to Asp-380, Leu-397 to Arg-412, Tyr-419 to Ala-426, Ser-467 to Lys-479.	S0152: 2, L0356: 2, S0356: 1, S0354: 1, S0360: 1, H0013: 1, H0581: 1, H0090: 1, H0641: 1, H0435: 1, H0648: 1, H0518: 1, H0479: 1, L0731: 1, S0031: 1 and H0542: 1.		
		965476	743	2 - 1252	1643	Lys-31 to Lys-42, Thr-63 to Glu-69, Thr-86 to Ile-98, Ala-110 to Lys-117, Pro-135 to Glu-145, Glu-152 to Glu-163, Asn-197 to Lys-202, Asp-209 to Lys-231, Leu-233 to Asp-239, Leu-256 to Arg-271, Tyr-278 to Ala-285, Ser-326 to Lys-338.			
		729290	744	49 - 240	1644	Ser-37 to Gly-44, Ile-46 to Glu-60.			
178	HDPBB41	1195686	188	2480 - 564	1088	Pro-6 to Cys-12, Val-15 to Gly-28, Arg-45 to Pro-53.	AR089: 6, AR061: 2 H0589: 2		
							AR089: 18, AR061: 6 L0803: 5, H0640: 2, H0373: 2, H0040: 2,		

	H0412: 2, S0422: 2, L0794: 2, L0804: 2, L0655: 2, H0547: 2, L0748: 2, L0777: 2, L0759: 2, H0543: 2, H0624: 1, S0116: 1, H0341: 1, S0418: 1, S0356: 1, S0358: 1, S0360: 1, H0329: 1, L0717: 1, T0039: 1, H0013: 1, H0427: 1, H0156: 1, L0021: 1, S0182: 1, H0263: 1, H0039: 1, T0086: 1, H0628: 1, H0591: 1, H0487: 1, H0102: 1, T0041: 1, T0042: 1, H0494: 1, S0142: 1, S0002: 1, L0662: 1, L0364: 1, L0774: 1, L0805: 1, L0809: 1, L0663: 1, H0144: 1, H0702: 1, H0519: 1, H0682: 1, H0684: 1, H0659: 1, H0660: 1, H0521: 1, H0696: 1, H0555: 1, L0751: 1, L0749: 1, L0758: 1, L0593: 1, H0668: 1 and H0667: 1.					
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		925800	745	2 - 667	1645	Asp-37 to Ile-44, Asp-47 to Thr-52, Pro-80 to Asp-85, Ala-90 to Tyr-101, Asp-138 to Glu-146, Ser-154 to Phe-161, Asn-172 to Gln-178, Gln-185 to Glu-190, Asn-205 to Ser-215.			
179	HEOPI32	907903	189	2 - 640	1089	Phe-8 to Asp-18, Pro-71 to Arg-84, Arg-90 to Asp-97, Ser-125 to Leu-133, Ala-137 to Gln-144, Met-181 to Gly-190, Gln-193 to Ile-199.	AR089: 1, AR061: 1 H0457: 5, L0766: 3, L0791: 2, S0420: 1, S0250: 1, L0638: 1, L0803: 1, L0806: 1, H0144: 1, H0547: 1, L0779: 1, L0485: 1 and H0423: 1.		
180	HFSAG03	1151479	190	716 - 360	1090		AR089: 18, AR061: 11 H0057: 1, L0520: 1 and L0389: 1.		
181	HFXCI24	960973	746	496 - 320	1646	Glu-33 to Thr-45, Arg-50 to Ser-59.			
		1182719	191	3 - 680	1091		AR061: 4, AR089: 2 H0361: 3, S0001: 1, S0045: 1, S0278: 1, S0144: 1 and S0053: 1.		
		908374	747	1 - 663	1647	Val-2 to Val-12, Asp-20 to Glu-26, Gln-56 to Gly-61, Gly-69 to Arg-76,			

182	HF ^X HJ89	907938	192	162 - 881	1092	Gly-167 to Lys-175, Pro-178 to Gly-205.	AR061: 4, AR089: 2 H0556: 1, H0650: 1, S0001: 1, S0376: 1, H0574: 1, S0346: 1, H0328: 1, L0649: 1, H0689: 1, H0660: 1, L0752: 1 and H0445: 1.			
183	HHPTC55	1106390	193	2 - 676	1093	Ile-26 to Arg-44, Ser-85 to Leu-93, Ala-97 to Gln-104, Ile-141 to Gly-149, Asp-172 to Gly-177.	AR089: 1, AR061: 1 H0265: 1, H0556: 1, H0477: 1, S0112: 1 and L0794: 1.			
184	HJBBP54	907951 1195070	748 194	1 - 435 3 - 575	1648 1094	Ala-18 to Arg-23, Phe-28 to Asn-33, Arg-79 to Lys-84, Arg-104 to Ser-112, Asn-181 to Thr-188. Ala-18 to Arg-23.	AR061: 193, AR089: 73 H0265: 1, H0050: 1, H0634: 1 and T0042: 1.			
185	HKAHB56	869621 1162649	749 195	3 - 575 674 - 1609	1649 1095	Gln-1 to His-6, Pro-9 to Leu-16, Trp-41 to His-47, His-49 to Val-57, Arg-103 to Gln-110, Glu-119 to Lys-125, Gln-173 to Gln-180, Pro-216 to Arg-226, Ile-281 to Ser-287.	AR061: 0, AR089: 0 L0751: 3, L0747: 3, H0662: 2, H0641: 2, L0749: 2, L0758: 2, S0114: 1, H0638: 1, S0046: 1, H0427: 1, H0618: 1, H0424: 1, H0553: 1, H0032: 1, H0494: 1, S0450: 1, L0773: 1, L0804: 1,			

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188	HNTRV07	1199546	752	1 - 501	1652	Met-62 to Lys-73, Thr-137 to Arg-142.	AR061: 1, AR089: 1 L0803: 5, L0665: 2, L0438: 2, L0758: 2, S0418: 1, L0717: 1, H0586: 1, H0622: 1, H0038: 1, L0662: 1, L0794: 1, L0783: 1, L0790: 1, L0664: 1, H0547: 1, H0519: 1, H0672: 1, H0539: 1, S0152: 1, L0740: 1, L0747: 1, L0777: 1 and S0242: 1.	L0759: 1 and H0542: 1.	
189	HODEX10	1104108	753	1 - 366	1653	Gln-15 to Lys-21, Arg-57 to His-72.	AR061: 6, AR089: 3 H0615: 5		
190	HOGAQ10	1222600	754	22 - 159	1654	Met-1 to Arg-6, Ser-16 to Lys-29.	AR089: 1, AR061: 0 S0422: 4, L0750: 4, L0766: 3, L0794: 2, S0242: 2, H0542: 2, H0170: 1, S0116: 1, H0675: 1, H0497: 1, H0486: 1, H0013: 1, H0090: 1, H0040: 1, H0551: 1, L0649: 1.		

191	HOSBW20	985056	201	1 - 927	1101	1655	Asp-40 to Gln-60, Phe-99 to Ser-104, Ser-109 to Gln-117, Lys-123 to Lys-137, Asn-175 to Pro-181.	AR061: 3, AR089: 2 S0206: 2, L0439: 2, S0222: 1, S0003: 1, H0428: 1, L0766: 1 and L0438: 1.	L0606: 1, H0519: 1, H0435: 1, L0779: 1, L0593: 1 and H0543: 1.
192	HRADL60	1151310	202	2765 - 1203	1102	1656	Val-41 to Asp-46, Met-64 to Arg-70, Arg-135 to Lys-146, Tyr-151 to Asn-157, Glu-167 to Ser-172.	AR089: 2, AR061: 1 L0777: 12, L0766: 9, L0803: 5, L0748: 5, L0752: 5, L0758: 5, L0759: 5, L0666: 4, L0794: 3, L0805: 3, L0743: 3, L0747: 3, S0222: 2, H0457: 2, S0003: 2, L0649: 2, L0804: 2, L0809: 2, L0663: 2, L0664: 2,	

	H0539: 2, L0744: 2, L0740: 2, L0596: 2, L0362: 2, S0026: 2, H0624: 1, H0170: 1, T0049: 1, H0402: 1, H0638: 1, S0420: 1, L0454: 1, S0356: 1, S0360: 1, H0637: 1, H0393: 1, L0717: 1, H0486: 1, T0082: 1, L0163: 1, H0594: 1, H0266: 1, H0416: 1, H0328: 1, H0622: 1, T0006: 1, H0553: 1, H0674: 1, H0163: 1, H0038: 1, H0634: 1, H0616: 1, H0551: 1, H0625: 1, H0538: 1, L0598: 1, L0770: 1, L0646: 1, L0764: 1, L0662: 1, L0375: 1, L0515: 1, L0659: 1, L0783: 1, L0789: 1, L0791: 1, T0068: 1, H0520: 1, H0684: 1, H0658: 1, H0518: 1, S0013: 1, S0146: 1, H0555: 1, L0779: 1, L0780: 1, L0757: 1 and S0462: 1	
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193	HSGSC29	1150837	757	68 - 1630	1657	Val-41 to Asp-46, Met-64 to Arg-70, Arg-135 to Lys-146, Tyr-151 to Asn-157, Glu-167 to Ser-172. Val-19 to His-24, Gly-88 to Gly-93, Pro-156 to Arg-169.	AR089: 5, AR061: 5 H0255: 4, H0593: 3, H0620: 2, H0448: 2, H0254: 1, S0358: 1, H0208: 1, H0592: 1 and H0272: 1.		
194	HTEDX38	1106208	758	327 - 749	1658	Leu-13 to Tyr-18, Tyr-108 to Gly-113.	AR061: 8, AR089: 5 L0794: 4, L0766: 4, L0758: 4, H0624: 3, H0038: 3, S0007: 2, H0616: 2, L0770: 2, L0803: 2, H0144: 2, L0751: 2, L0747: 2, L0750: 2, H0170: 1, T0049: 1, S0376: 1, S0045: 1, H0553: 1, H0040: 1, T0042: 1, H0646: 1, L0768: 1, L0655: 1, L0787: 1, L0788: 1, L0666: 1, L0665: 1, H0520: 1, S0126: 1, H0435: 1, S0378: 1, L0720: 1,		

195	HTEJE15	920697	759	3 - 1436	1659	Gln-124 to Arg-135, Ser-149 to Ser-154, Lys-161 to Ser-176, Ala-184 to Val-204, Pro-207 to His-216, Tyr-270 to Gln-281, Ser-300 to Tyr-327, Gly-330 to Asp-346, Gln-352 to Glu-367, Gly-380 to Ser-397, Gln-401 to Trp-409, Phe-420 to Tyr-435, Ala-453 to Ser-458.	H0555: 1, L0779: 1, L0777: 1 and S0192: 1.		
		1102531	205	1 - 405	1105	Arg-38 to Thr-48, Asp-107 to Thr-114, Ser-123 to Asp-135.			
196	HTOES03	908360	760	2 - 319	1660		AR061: 4, AR089: 1 L0758: 7, L0794: 4, H0038: 2 and L0791: 1.		
		1150877	206	2 - 1186	1106	Ala-1 to Ala-8, Ala-11 to Ser-22, Gln-86 to Ala-92, Asp-156 to Leu-167, Arg-169 to Arg-176, Glu-325 to Ala-332, Asp-354 to Leu-360, Ser-387 to Lys-395.			
		955814	761	3 - 1022	1661	Arg-1 to His-8, Gln-27 to Ala-33, Asp-97 to Leu-108,	AR089: 1, AR061: 0 L0766: 7, H0561: 2, L0774: 2, L0777: 2, H0052: 1, H0264: 1, H0625: 1, L0761: 1, L0806: 1, L0776: 1, L0790: 1, L0793: 1, L0779: 1 and L0752: 1.		

197	HTOHS18	1193057	207	3 - 1070	1107	Arg-110 to Arg-117, Glu-266 to Ala-273, Asp-295 to Leu-301, Ser-328 to Ala-340. Cys-10 to Gln-16, Gly-66 to Arg-72, Asp-170 to Trp-178, His-207 to Arg-212, Thr-265 to Lys-270, Lys-274 to Lys-285, Lys-306 to Gly-314, Phe-331 to Val-356.	AR061: 3, AR089: 1 L0777: 7, H0486: 3, L0659: 3, H0436: 2, L0731: 2, L0758: 2, H0171: 1, S0134: 1, H0657: 1, H0662: 1, L0717: 1, H0592: 1, H0485: 1, H0581: 1, H0264: 1, H0100: 1, H0633: 1, L0763: 1, L0770: 1, L0637: 1, L0772: 1, L0764: 1, L0662: 1, L0805: 1, L0776: 1, L0655: 1, L0783: 1, H0659: 1, L0612: 1, L0749: 1, L0750: 1 and H0352: 1.		
198	HWAAX38	908347 943936	762 208	2 - 592 3 - 404	1662 1108	Cys-5 to Gln-11. Ala-21 to Gln-27.	AR089: 5, AR061: 2 H0423: 6, H0556: 4, H0486: 4, H0271: 4, S0134: 3, H0657: 3, H0125: 3, S0278: 3, H0581: 3, L0768: 3, S0330: 3, H0134: 3, H0436: 3, H0445: 3,		

	H0542: 3, H0422: 3, H0265: 2, S0114: 2, S0218: 2, H0656: 2, S0360: 2, H0250: 2, H0069: 2, H0090: 2, H0264: 2, S0142: 2, L0766: 2, L0775: 2, H0518: 2, H0576: 2, L0740: 2, L0777: 2, H0543: 2, T0002: 1, H0221: 1, H0220: 1, H0140: 1, H0255: 1, H0638: 1, H0608: 1, H0318: 1, L0471: 1, S0214: 1, H0428: 1, H0039: 1, H0087: 1, H0272: 1, H0056: 1, T0041: 1, S0450: 1, S0144: 1, S0344: 1, L0762: 1, L0770: 1, L0769: 1, L0761: 1, L0667: 1, L0774: 1, L0806: 1, L0776: 1, L0655: 1, L0607: 1, L0661: 1, L0659: 1, L0809: 1, L0787: 1, L0664: 1, S0052: 1, S0053: 1, H0698: 1, H0701: 1, H0539: 1, S0378: 1, L0748: 1, L0750: 1, L0756: 1.					
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199	HMSFN70	1210794	209	1 - 921	1109	Gly-25 to Arg-33, Glu-40 to Thr-55, Asp-125 to Lys-136, Val-174 to Pro-185, Pro-228 to Ala-235, Glu-270 to Gly-275, Pro-299 to Lys-307.	L0779: 1, L0755: 1 and H0136: 1. AR061: 4, AR089: 3 L0759: 7, L0731: 6, L0769: 4, L0766: 4, L0742: 3, L0751: 3, L0752: 3, H0624: 2, S6026: 2, L0770: 2, L0803: 2, L0774: 2, L0666: 2, H0670: 2, H0521: 2, L0754: 2, L0750: 2, L0777: 2, L0753: 2, L0757: 2, H0171: 1, H0650: 1, H0341: 1, H0675: 1, H0580: 1, H0574: 1, H0013: 1, H0052: 1, H0051: 1, H0083: 1, S6028: 1, S0003: 1, L0483: 1, H0644: 1, H0628: 1, H0038: 1, S0002: 1, L0772: 1, L0764: 1, L0768: 1, L0794: 1, L0806: 1, L0805: 1, L0776: 1, L0807: 1, L0656: 1, L0789: 1, H0689: 1, H0672: 1, H0555: 1, S0027: 1, L0756: 1, L0779: 1, L0755: 1 and		
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									L0758: 1.		
200	HUSGB93	921879 1224029	763 210	1 - 921 363 - 983	1663 1110				AR089: 98, AR061: 8 S0126: 2, H0341: 1, H0412: 1, L0387: 1, L0766: 1, L0379: 1, L0559: 1, S0374: 1 and S0434: 1.		
		923014	764	2 - 520	1664	Arg-1 to Gly-8, Pro-18 to Gly-25, Thr-60 to Leu-67, Gly-107 to Thr-113.					
201	HELHL56	1164004	211	2 - 943	1111	Ser-10 to Ser-16, Lys-226 to Trp-231, Thr-288 to Ser-300.			AR061: 4, AR089: 2 S0426: 3, L0766: 3, S0126: 2, S0282: 1, S0354: 1, S0376: 1, S0045: 1, H0486: 1, H0178: 1, S0003: 1, H0622: 1, H0591: 1, H0040: 1, H0551: 1, H0647: 1, L0761: 1, L0651: 1, S0152: 1, H0521: 1, H0522: 1, S0028: 1, L0754: 1, L0757: 1, L0592: 1 and H0542: 1.		
		578441	765	2 - 307	1665	Ser-10 to Ser-16, Phe-89 to Ser-97.					
202	HOENY85	1191756	212	2 - 1357	1112				AR061: 5, AR089: 2 S0354: 1, S0045: 1.		

203	HTEHI14	875830	766	2 - 664	1666	Lys-133 to Trp-138, Thr-195 to Gln-206.	H0178: 1, H0622: 1, H0591: 1, H0040: 1, H0647: 1, L0766: 1, S0126: 1, S0152: 1, H0521: 1, S0028: 1, L0754: 1, L0592: 1 and H0542: 1.	AR089: 5, AR061: 5 H0038: 4	
		1102680	213	209 - 541	1113	Asp-57 to Lys-62.			
		526687	767	216 - 458	1667				
204	HETDT70	1228235	214	1 - 588	1114	Gly-33 to Asp-45, Ser-78 to Gly-85.	AR089: 153, AR061: 40 H0648: 138, L0666: 63, L0595: 48, L0662: 47, L0663: 47, S0360: 45, H0670: 44, H0659: 43, L0659: 41, L0526: 39, S0358: 37, L0664: 35, L0717: 31, L0775: 31, H0657: 30, L0750: 30, T0010: 29, L0655: 29, L0665: 27, H0543: 27, L0598: 23, H0672: 23, S0330: 23, H0170: 21, L0351: 21, L0520: 21, L0646: 19, L0521: 19, L0752: 19, S0380: 18, L0596: 18, L0361:		

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 H0188: 6, H0059: 6,
 L0641: 6, L0522: 6,
 L0783: 6, H0435: 6,
 H0576: 6, L0589: 6,
 L0581: 6, L0599: 6,
 S0116: 5, S0356: 5,
 S0007: 5, S0045: 5,
 H0351: 5, H0597: 5,
 H0014: 5, S0388: 5,
 S0250: 5, H0625: 5,
 S0426: 5, L0637: 5,
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 H0545: 4, H0046: 4,
 H0009: 4, H0012: 4,
 H0057: 4, H0688: 4,
 T0006: 4, H0674: 4,
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 L0767: 4, L0768: 4,
 L0650: 4, L0527: 4,
 L0530: 4, H0518: 4,
 L0592: 4, L0608: 4,
 L0603: 4, S0026: 4,

	S0242: 4, H0542: 4, H0395: 3, S0040: 3, H0341: 3, S0282: 3, H0255: 3, H0663: 3, H0662: 3, H0306: 3, H0208: 3, H0393: 3, H0640: 3, H0586: 3, H0587: 3, H0150: 3, H0123: 3, H0024: 3, S0316: 3, H0617: 3, H0032: 3, H0068: 3, H0135: 3, H0561: 3, L0625: 3, L0501: 3, L0606: 3, L0519: 3, L0438: 3, H0660: 3, H0134: 3, H0187: 3, S0392: 3, L0754: 3, L0731: 3, H0667: 3, H0171: 2, H0394: 2, S0342: 2, S0134: 2, H0583: 2, H0656: 2, L0416: 2, L0760: 2, H0669: 2, H0661: 2, S0444: 2, H0637: 2, S0468: 2, H0619: 2, H0441: 2, H0333: 2, H0485: 2, T0039: 2, H0318: 2, H0546: 2, N0006: 2, H0565: 2, H0242: 2, T0003: 2, H0015: 2, H0373: 2,					
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207	HMSHI83	1204709	217	2 - 1720	1117	Arg-59 to Thr-65, Gln-78 to Lys-83, Tyr-211 to Leu-223, Leu-255 to Phe-265, Gly-320 to Lys-328, Arg-343 to Phe-354, Pro-533 to Ser-553.	Arg-98 to Thr-104, Gln-117 to Lys-122.	H0522: 1, H0555: 1, H0478: 1, L0744: 1, L0750: 1, L0731: 1, H0423: 1 and S0424: 1.		
		963126	769	102 - 620	1669			AR089: 4, AR061: 3 L0439: 13, L0748: 7, H0591: 4, L0770: 4, L0779: 4, L0777: 4, H0622: 3, H0560: 3, L0794: 3, L0518: 3, L0752: 3, L0588: 3, S0376: 2, H0013: 2, H0581: 2, H0231: 2, L0163: 2, H0090: 2, H0623: 2, S0142: 2, L0772: 2, L0766: 2, L0655: 2, L0665: 2, H0144: 2, L0565: 2, L0352: 2, H0689: 2, L0758: 2, L0759: 2, H0542: 2, T0002: 1, H0657: 1, S0116: 1, H0341: 1, S0212: 1, H0638: 1, S0007: 1, H0619: 1, H0411: 1, S0278: 1, H0497: 1, H0486: 1, H0635: 1, H0156: 1, H0046: 1.		

208	HTEPM45	963083	770	2 - 841	1670	Arg-59 to Thr-65, Gln-78 to Lys-83, Tyr-211 to Leu-223, Glu-257 to Lys-262.	H0051: 1, S6028: 1, S0003: 1, H0551: 1, H0509: 1, H0641: 1, H0646: 1, S0002: 1, H0529: 1, L0640: 1, L0639: 1, L0768: 1, L0804: 1, L0651: 1, L0659: 1, L0809: 1, L0788: 1, L0663: 1, H0701: 1, H0703: 1, S0374: 1, H0547: 1, H0522: 1, H0555: 1, H0478: 1, L0744: 1, L0750: 1, L0731: 1, H0423: 1 and S0424: 1.		
		952389	218	3 - 1229	1118	Arg-1 to Cys-9, Tyr-47 to Leu-59, Leu-91 to Phe-101, Gly-156 to Lys-164, Arg-179 to Phe-190, Pro-369 to Ser-389.	AR089: 9, AR061: 7 H0486: 102, S0360: 76, L0598: 39, H0251: 35, L0659: 32, H0144: 32, H0013: 31, H0624: 28, H0024: 26, H0050: 25, L0471: 25, L0662: 22, L0748: 22, H0619: 20, H0123: 20, S0003: 18, H0031: 15, H0170: 14, H0124: 14, H0328:		

13, L0750: 13, H0644:	
12, S0126: 12, S0028:	
11, L0757: 11, S0196:	
11, H0587: 10, S0214:	
10, L0589: 10, S0040: 9,	
H0622: 9, L0731: 9,	
H0171: 8, S0356: 8,	
L0717: 8, H0586: 8,	
H0620: 8, H0252: 8,	
H0551: 8, H0352: 8,	
H0661: 7, H0081: 7,	
L0747: 7, L0755: 7,	
S0358: 6, H0598: 6,	
L0646: 6, L0771: 6,	
S3014: 6, H0343: 6,	
H0595: 6, S0212: 5,	
H0329: 5, H0208: 5,	
H0574: 5, H0316: 5,	
H0100: 5, L0666: 5,	
L0565: 5, H0658: 5,	
S0390: 5, S0027: 5,	
S0011: 5, S0192: 5,	
S0194: 5, S0376: 4,	
H0575: 4, H0039: 4,	
H0628: 4, H0090: 4, : 4,	
L0663: 4, L0664: 4,	
S0374: 4, S0380: 4,	
L0744: 4, S0242: 4,	
H0295: 3, H0645: 3,	
H0411: 3, H0546: 3,	
H0012: 3, S0250: 3,	

	L0768: 3, L0375: 3, H0684: 3, H0672: 3, S0332: 3, L0754: 3, H0294: 2, H0663: 2, H0592: 2, S0005: 2, H0333: 2, H0632: 2, H0485: 2, T0060: 2, H0599: 2, H0309: 2, H0544: 2, H0545: 2, H0041: 2, H0375: 2, H0553: 2, L0142: 2, H0647: 2, L0776: 2, L0665: 2, H0648: 2, S0330: 2, S0378: 2, S0206: 2, S0032: 2, L0751: 2, H0668: 2, S0384: 2, H0506: 2, L0615: 1, S0342: 1, H0381: 1, S0116: 1, S0001: 1, H0664: 1, H0125: 1, S0354: 1, T0008: 1, H0640: 1, H0370: 1, H0391: 1, T0039: 1, H0101: 1, H0245: 1, H0156: 1, L0021: 1, H0122: 1, H0318: 1, H0231: 1, H0049: 1, T0003: 1, H0051: 1, H0286: 1, H0364: 1, H0428: 1, T0023: 1, I0143: 1	
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211	HHEDC90	1226157	221	192 - 3269	1121	Arg-8 to Lys-19, Gln-75 to Pro-84, Ser-112 to Ser-120, Asn-132 to Glu-138, Ala-159 to Lys-172, Arg-217 to Gln-223, Asp-254 to Ser-259, Glu-297 to Gln-304, Pro-385 to Lys-395, Tyr-422 to Leu-427, Gln-438 to Glu-446, Arg-500 to Leu-510, Leu-555 to Thr-562, Pro-568 to Asp-573, Ser-648 to Ser-653, Ala-770 to Gly-777, Trp-803 to Leu-808, Leu-833 to Trp-843, Ala-851 to Thr-856, Lys-866 to Gly-873, Leu-904 to Arg-911, Arg-953 to Arg-961, Cys-973 to Arg-978, Pro-1003 to Arg-1016.	AR061: 3, AR089: 3, H0250: 4, L0766: 4, H0543: 4, H0559: 3, H0306: 2, H0635: 2, H0641: 2, H0521: 2, L0779: 2, H0542: 2, H0423: 2, H0556: 1, H0402: 1, L0468: 1, H0190: 1, H0069: 1, H0581: 1, H0087: 1, T0041: 1, L0761: 1, L0768: 1, S0053: 1, H0672: 1 and H0422: 1.		
		911447	774	1 - 687	1674	His-1 to Leu-7, Leu-52 to Thr-59, Pro-65 to Asp-70, Ser-145 to Ser-150.			
212	HNBRB59	685902	222	28 - 339	1122	Ala-47 to Gly-55.	H0026: 1, L0560: 1, L0378: 1 and H0595: 1.		

213	HNBNB116	965414	775	1 - 237	1675	Asn-17 to Lys-25, Arg-40 to Glu-46, Lys-64 to His-75. Arg-12 to Val-20, Gln-43 to Glu-51.	AR089: 1, AR061: 1 H0521: 4, H0650: 3, H0677: 3, H0656: 2, H0069: 2, H0581: 2, H0542: 2, H0423: 2, H0255: 1, L0539: 1, S0358: 1, H0575: 1, H0457: 1, H0083: 1, H0063: 1, H0560: 1, S0002: 1, H0529: 1, H0697: 1, H0543: 1 and H0422: 1.
214	HUJCL61	1223496	224	135 - 2861	1124	Arg-8 to Lys-19, Gln-75 to Pro-84, Ser-112 to Ser-120, Asn-132 to Glu-138, Ala-159 to Lys-172, Arg-217 to Gln-223, Asp-254 to Ser-259, Glu-297 to Gln-304, Pro-385 to Lys-395, Tyr-422 to Leu-427, Gln-438 to Glu-446, Arg-500 to Leu-510, Leu-555 to Thr-562, Pro-568 to Asp-573, Ser-648 to Ser-653	AR089: 3, AR061: 1 L0766: 6, H0521: 6, H0250: 5, H0543: 5, H0559: 4, H0581: 4, L0761: 4, L0779: 4, H0542: 4, H0650: 3, H0306: 3, H0069: 3, H0023: 3, H0423: 3, H0422: 3, H0677: 3, H0656: 2, H0255: 2, H0257: 2, H0635: 2, H0560: 2, H0641: 2, L0789: 2, L0777: 2, H0556: 1, H0402: 1, L0539: 1, S0358: 1

							Ala-770 to Gly-777, Trp-803 to Leu-808, Leu-833 to Trp-843, Ala-851 to Thr-856, Gln-863 to Trp-873, Cys-883 to Arg-901.	L0468: 1, H0190: 1, H0575: 1, H0457: 1, H0083: 1, H0063: 1, H0087: 1, T0041: 1, S0002: 1, H0695: 1, H0529: 1, L0764: 1, L0768: 1, S0053: 1, H0697: 1, H0702: 1, H0658: 1, H0672: 1, L0731: 1 and H0445: 1.		
215	HWLRC68	1089187	911432	776	116 - 715	1676	Arg-8 to Lys-19, Gln-75 to Pro-84, Ser-112 to Ser-120.	AR061: 2, AR089: 1 S0360: 1, S0132: 1 and H0412: 1.		
216	HFXFH42	1228147	911481	777	210 - 548	1677	Glu-65 to Arg-72.	AR061: 1, AR089: 0 L0770: 2, L0803: 2, L0439: 2, L0740: 2, L0731: 2, S0001: 1, H0373: 1, L0638: 1, L0766: 1, L0655: 1, L0787: 1, L0788: 1, L0745: 1, L0755: 1 and L0366: 1.		
217	HEQAN73	958912	713795	778	220 - 399	1678	Glu-28 to Phe-33, His-47 to Ser-53.	AR089: 6, AR061: 3 L0439: 6, L0804: 4,		
				227	12 - 878	1127				

								L0794: 3, L0756: 3, L0779: 3, H0125: 2, H0599: 2, H0544: 2, H0046: 2, L0764: 2, L0766: 2, L0803: 2, L0438: 2, H0521: 2, L0731: 2, S0452: 2, S0045: 1, S0046: 1, H0549: 1, H0575: 1, H0374: 1, H0194: 1, H0545: 1, H0083: 1, S0003: 1, H0328: 1, T0006: 1, H0623: 1, L0761: 1, L0768: 1, L0775: 1, L0806: 1, L0805: 1, L0666: 1, L0663: 1, H0520: 1, H0519: 1, H0682: 1, S0380: 1, H0445: 1, H0542: 1 and H0506: 1.		
218	HSLFS31	1106294	228	575 - 252	1128	Met-1 to Glu-14, Thr-73 to Glu-81, Ala-86 to Ile-96.	AR061: 5, AR089: 3 S0044: 1 and S0028: 1.			
219	HELK56	921511	779	3 - 215	1679	Glu-31 to Leu-36.	AR061: 3, AR089: 1 S0045: 1			
		1103702	229	575 - 33	1129					
		925698	780	129 - 788	1680					
220	HAMFW05	957586	230	1 - 558	1130	Asp-1 to Gly-9, Asp-86 to Glu-91, Pro-97 to Gly-103.	AR089: 13, AR061: 2 H0521: 6, L0757: 5, L0749: 4 L0779: 4			

Lys-115 to Asn-121, Pro-159 to Arg-166, Pro-168 to His-173.	H0620: 3, S0040: 2, S0342: 2, H0305: 2, S0418: 2, S0132: 2, H0551: 2, H0412: 2, S0344: 2, L0776: 2, L0659: 2, L0740: 2, L0747: 2, L0752: 2, H0542: 2, T0049: 1, H0656: 1, S0001: 1, H0306: 1, S0360: 1, S0046: 1, H0619: 1, H0370: 1, H0559: 1, H0590: 1, H0266: 1, H0288: 1, H0286: 1, H0252: 1, H0213: 1, H0673: 1, H0116: 1, H0433: 1, H0623: 1, H0560: 1, H0652: 1, S0002: 1, H0529: 1, L0762: 1, L0763: 1, L0772: 1, L0646: 1, L0764: 1, L0765: 1, L0662: 1, L0766: 1, L0526: 1, L0783: 1, L0789: 1, S0126: 1, H0435: 1, H0539: 1, S0152: 1, H0522: 1, H0555: 1, S014: 1, L0777: 1, L0731: 1, L0758: 1, S0031: 1, S0011: 1 and S0446: 1.
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221	HTEDG81	1193054	231	70 - 828	1131	Leu-58 to Val-64, Lys-120 to Phe-132, Tyr-150 to Thr-157, Glu-178 to Glu-183, Arg-217 to Leu-222, Glu-236 to Ser-252.	AR089: 2, AR061: 2 H0038: 3, L0758: 2, H0616: 1 and T0042: 1.		
		772995	781	75 - 497	1681	Leu-58 to Val-64.			
222	HAMGO24	943287	232	2 - 550	1132	Asp-10 to Phe-15, Ser-57 to Leu-62, Lys-77 to Val-83.	AR089: 2, AR061: 1 L0766: 9, L0742: 6, S0358: 3, L0803: 3, H0521: 3, L0777: 3, L0758: 3, H0413: 2, S0466: 2, L0775: 2, L0666: 2, L0779: 2, L0752: 2, S0360: 1, H0393: 1, H0587: 1, H0486: 1, H0013: 1, H0069: 1, H0575: 1, H0052: 1, H0545: 1, H0510: 1, S0003: 1, H0553: 1, H0560: 1, H0509: 1, S0422: 1, L0598: 1, L0762: 1, L0794: 1, L0804: 1, L0664: 1, H0519: 1, H0522: 1, L0755: 1, S0031: 1 and H0653: 1.		
223	HMWBH91	1193044	233	249 - 1298	1133	Glu-13 to Ser-19, Lys-45 to Pro-50, Ser-89 to Gly-96,	AR061: 2, AR089: 2 L0777: 8, L0779: 5, L0646: 3, L0803: 3,		

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224	HOECH19	965639	234	140 - 934	1134	Pro-314 to Phe-319, Asn-322 to Asn-327, Gly-366 to Lys-372, Ile-388 to Ala-395, Glu-402 to Arg-407. Ala-5 to Ser-11, Ser-101 to Asn-112.	AR061: 8, AR089: 3 L0759: 9, L0758: 8, L0439: 5, L0163: 4, L0809: 4, L0779: 4, L0770: 3, L0750: 3, L0777: 3, H0063: 2, L0794: 2, L0766: 2, L0659: 2, L0438: 2, S0126: 2, H0666: 2, L0747: 2, L0757: 2, H0542: 2, H0656: 1, L0785: 1, H0574: 1, L0105: 1, H0687: 1, H0644: 1, H0038: 1, H0616: 1, L0475: 1, L0520: 1, L0769: 1, L0646: 1, L0764: 1, L0803: 1, L0774: 1, L0775: 1, L0776: 1, L0655: 1, L0559: 1, L0663: 1, L0665: 1, H0684: 1, S0152: 1, H0555: 1, L0751: 1, L0749: 1, L0755: 1, L0731: 1, S0434: 1		
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225	HSRAA80	1121919	235	2 - 379	1135	Ile-1 to Cys-10, Arg-95 to Arg-104.	S0242: 1, H0543: 1, H0422: 1 and S0412: 1. AR061: 150, AR089: 93 S0011: 1		
		937640	783	2 - 325	1683	Ile-1 to Cys-10, Arg-95 to Phe-106.			
226	HHEDF50	1174682	236	5 - 502	1136		AR089: 3, AR061: 1 H0542: 40, H0543: 10, H0580: 4, H0592: 4, H0510: 4, H0593: 4, H0521: 4, H0551: 3, H0509: 3, H0519: 3, H0650: 2, H0586: 2, H0587: 2, H0544: 2, H0546: 2, H0545: 2, H0522: 2, H0555: 2, H0583: 1, H0602: 1, H0581: 1, H0488: 1, H0689: 1, H0528: 1 and H0694: 1.		
		974396	784	5 - 502	1684				
227	HHEMK34	974395	237	29 - 277	1137	Gln-1 to Val-8.	AR061: 1, AR089: 1 H0542: 40, H0543: 10, H0580: 4, H0592: 4, H0510: 4, H0593: 4, H0521: 4, H0551: 3, H0509: 3, H0519: 3, H0650: 2, H0586: 2, H0587: 2, H0544: 2,		

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228	HMAGK69	1105451	238	556 - 77	1138	Ala-3 to Gly-9, Lys-36 to Glu-42, Ala-49 to Glu-55, Ser-90 to Gln-102, His-134 to Trp-139.			AR089: 2, AR061: 1, S0278: 1 and S0052: 1.			
		723186	785	31 - 417	1685	Arg-1 to Ser-6, Lys-23 to Glu-29, Ala-36 to Glu-42, Ser-77 to Gln-89.						
229	HNGNW52	1132300	239	939 - 43	1139	Leu-25 to Ala-31, Ala-102 to Ala-108, Ser-285 to Gly-290.			AR089: 37, AR061: 13 S0050: 1, H0031: 1, S0428: 1, S0028: 1, S0031: 1 and S0260: 1.			
		883074	786	38 - 1009	1686							
230	H6EDK67	974775	240	75 - 668	1140	Lys-29 to Arg-34, Glu-121 to Asp-126, Lys-132 to Asp-155.			AR089: 24, AR061: 7 L0777: 5, S0116: 3, L0809: 3, H0696: 3, H0423: 3, S0282: 2, S0354: 2, H0083: 2, H0316: 2, L0763: 2, L0767: 2, L0805: 2, L0776: 2, L0779: 2, S0114: 1, H0657: 1, H0656: 1, S0358: 1,			

231	HWBCS43	1151532	241	125 - 880	1141	Ser-13 to Gln-29, Pro-31 to Lys-38, Asp-82 to Gln-90, His-175 to Gly-180, Thr-186 to Gly-202.	S0360: 1, H0340: 1, S0046: 1, H0619: 1, H0455: 1, H0333: 1, H0574: 1, H0559: 1, T0109: 1, H0156: 1, L0021: 1, T0074: 1, H0318: 1, S0474: 1, S0049: 1, H0327: 1, H0530: 1, H0615: 1, H0553: 1, H0673: 1, H0059: 1, L0065: 1, H0207: 1, L0520: 1, L0769: 1, L0761: 1, L0521: 1, L0774: 1, L0655: 1, L0659: 1, L0526: 1, L0666: 1, L0664: 1, H0659: 1, H0518: 1, S0176: 1, H0478: 1, L0748: 1, L0750: 1, L0755: 1, L0731: 1, S0436: 1, L0608: 1, L0362: 1, S0026: 1 and S0242: 1. AR089: 16, AR061: 3 L0747: 11, L0731: 8, L0740: 7, L0361: 6, H0657: 5, H0658: 5, H0542: 5, H0494: 4, L0770: 4, L0772: 4, L0766: 4, L0748: 4.		
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232	HCE3H71	961681	787	285 - 737	1687	Asp-29 to Gln-37.		AR089: 14, AR061: 10 L0439: 12, L0438: 5, L0741: 4, H0052: 2, H0009: 2, L0769: 2, L0794: 2, H0229: 1, H0572: 1, L0770: 1, L0796: 1, L0789: 1 and L0786: 1.		
233	HOFMS43	947973	243	3 - 359	1143	Asp-1 to Asp-17, Pro-61 to Asn-66, Tyr-84 to Tyr-90, Ser-103 to Trp-110.		AR051: 15, AR050: 9, AR089: 7, AR061: 5, AR054: 1 H0415: 1		
234	HOVCO14	947999	244	3 - 539	1144	Arg-78 to His-85, Leu-99 to Lys-104, Lys-123 to His-132, Ser-157 to Pro-174.		AR089: 3, AR061: 2 S6016: 1 and H0428: 1.		
235	HTOBE75	1161571	245	3 - 1067	1145	Gly-53 to Thr-60, Ser-72 to Ser-88.		AR061: 2, AR089: 1 H0038: 3, L0748: 3.		

236	HCMSL08	591896	788	1 - 414	1688					L0659: 2, L0743: 2, L0744: 2, H0486: 1, H0421: 1, H0024: 1, H0031: 1, H0272: 1, L0662: 1, L0384: 1, L0809: 1 and L0779: 1.			
		898203	246	1 - 1221	1146	Gly-1 to Thr-10, Ala-14 to Gly-19, Pro-52 to Val-57, Pro-85 to Gln-95, Lys-198 to His-204, Pro-254 to Glu-260, Glu-269 to Ser-282, Glu-302 to Gly-307, Asp-320 to Asp-326, Asp-373 to Ser-380, Ile-396 to Asp-407.				AR051: 86, AR054: 73, AR050: 67, AR089: 10, AR061: 5 H0706: 8, S0366: 5, S0364: 4, L0485: 4, L0604: 4, L0777: 3, L0623: 2, S0362: 2, H0373: 2, L0520: 2, L0747: 2, H0624: 1, H0619: 1, H0550: 1, H0196: 1, L0646: 1, L0809: 1, H0693: 1, S0328: 1 and H0214: 1.			104770, 107670, 110700, 135940, 145001, 146790, 152445, 152445, 159001, 174000, 179755, 182860, 182860, 182860, 191315, 230800, 230800, 266200, 600897, 601105, 601412, 601652, 602491

		959176	789	1372 - 569	1689	Lys-59 to His-65, Pro-115 to Glu-121, Glu-130 to Ser-143, Glu-163 to Gly-168, Asp-181 to Asp-187, Asp-234 to Ser-241, Ile-257 to Asp-268.				
237	HDPBS64	846624	247	2 - 685	1147	Phe-7 to Pro-15, Trp-34 to Gly-40.	AR089: 1, AR061: 0 S0222: 1, S0002: 1, L0804: 1, L0663: 1 and H0521: 1.			
238	HDTBR50	846630	248	130 - 342	1148	Ala-2 to Glu-7, Arg-50 to Glu-58.	AR089: 41, AR061: 4 H0486: 2			
239	HTDAB17	890384	249	3 - 605	1149	Asp-1 to Gly-14, Ala-60 to Lys-71, Gln-101 to Glu-118.	AR089: 1, AR061: 0 L0747: 28, L0588: 22, L0757: 19, H0251: 15, S0358: 14, S0045: 13, L0731: 12, H0551: 10, H0412: 10, L0771: 10, L0748: 9, L0758: 9, H0506: 9, H0556: 8, S0046: 8, H0622: 8, H0013: 7, H0623: 7, L0662: 7, S0192: 7, S0003: 6, L0659: 6, L0666: 6, S0328: 6, L0439: 6, L0750: 6, L0759: 6, L0599: 6, L0608: 6, S0040: 5, S0360: 5, H0581: 5,	6p24-p23	125264, 134570, 600511, 601556	

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240	HABAE22	1227053	250	1086 - 1	1150	Gly-8 to Gly-13, Ala-76 to Ala-81, Arg-154 to Gly-159, Arg-338 to Pro-349.			AR089: 1, AR061: 0 H0617: 10, L0743: 4, S0358: 3, H0618: 3, H0052: 3, H0687: 3, H0135: 3, H0494: 3, L0646: 3, L0750: 3, L0731: 3, L0757: 3, L0601: 3, H0484: 2, H0662: 2, S0418: 2, H0549: 2, H0599: 2, H0150: 2, H0181: 2, H0087: 2, H0412: 2, H0529: 2, L0769: 2, L0649: 2, L0775: 2, L0663: 2, H0547: 2, L0742: 2, H0543: 2, H0556: 1, H0686: 1, H0685: 1, S0134: 1, S0218: 1, H0483: 1, H0661: 1, H0664: 1, S0360: 1, S0046: 1,		

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241	HE9MI70	1217048	965314	790	3 - 767	1690	Arg-1 to Ala-6, Glu-28 to Ala-34, Gln-41 to Gly-70, Ala-161 to Phe-168, Lys-180 to Arg-191, His-193 to Leu-198, Glu-216 to Asp-227. Gln-1 to Arg-8, Glu-68 to Glu-74, Tyr-93 to Gln-99, Gly-119 to Val-124, Glu-149 to His-154, Asp-178 to Asp-183, Pro-231 to Leu-241.	AR089: 21, AR061: 7 S0126: 3, L0163: 2, S0426: 2, H0547: 2, L0439: 2, L0751: 2, S0418: 1, S0468: 1, L0471: 1, S0051: 1, H0673: 1, L0637: 1, L0794: 1, L0663: 1, H0144: 1, S0027: 1, L0752: 1, L0757: 1 and H0444: 1.
242	HHFDK15	1147850	953319	791	1 - 684	1691	Ser-24 to Ser-38, Pro-72 to Gly-97, Lys-146 to His-153, Ser-173 to Ser-182, Leu-192 to Gln-201.	AR061: 72, AR089: 44 L0438: 7, L0805: 4, L0779: 4, L0439: 3, H0619: 2, S0010: 2, L0766: 2, L0809: 2, L0754: 2, L0755: 2, L0594: 2, L0601: 2, H0422: 2, S0430: 1, H0656: 1, H0484: 1, S0360: 1, S0222: 1, H0581: 1, H0327: 1.

243	HOSNZ11	854734	792	3 - 380	1692	Gly-17 to Thr-26, Glu-93 to Asp-101, Arg-117 to Ala-125.	H0050: 1, L0471: 1, H0644: 1, L0768: 1, L0794: 1, L0774: 1, L0776: 1, L0636: 1, L0787: 1, L0665: 1, H0672: 1, H0696: 1, L0751: 1, L0780: 1, L0608: 1, S0194: 1 and H0677: 1.		
		1162664	253	2 - 481	1153	Gln-10 to Thr-18, Ser-40 to Lys-47, Lys-59 to Lys-64, Lys-73 to Leu-82, Asp-145 to Thr-160.	AR061: 6, AR089: 2 L0439: 4, L0770: 2, L0794: 2, L0438: 2, L0740: 2, H0599: 1, T0082: 1, S0003: 1, H0644: 1, L0639: 1, S3014: 1, S0028: 1, S0206: 1, L0756: 1, L0779: 1 and L0752: 1.		
244	HTAEW05	965875 1151514	793 254	3 - 461 98 - 817	1693 1154	Ala-27 to Ala-36, Glu-41 to Asp-48, Asp-84 to Lys-92, Ala-140 to Glu-145, Leu-168 to Glu-173, Gln-213 to Ser-218.	AR089: 11, AR061: 7 L0766: 3, L0617: 1, H0069: 1, H0318: 1, H0050: 1, S0250: 1, L0804: 1, L0663: 1, L0750: 1, L0786: 1, L0752: 1 and L0592: 1.		
		838562	794	91 - 615	1694	Ala-27 to Ala-36			

245	HTTKN45	1181807	255	249 - 1772	1155	Glu-41 to Asp-48, Asp-84 to Lys-92, Ala-140 to Glu-145. Gln-2 to Ala-11, Pro-23 to Gly-32, Lys-38 to Gln-52, Thr-57 to Ser-64, Thr-72 to Ala-78, Asp-88 to Asp-93, Lys-107 to Gln-126.	AR089: 6, AR061: 6 H0634: 4, H0547: 3, H0521: 3, H0224: 2, H0208: 2, H0040: 2, H0529: 2, H0144: 2, H0656: 1, S0356: 1, H0600: 1, T0039: 1, H0013: 1, T0110: 1, H0046: 1, H0266: 1, H0032: 1, H0090: 1, H0038: 1, H0551: 1, T0041: 1, T0042: 1, H0509: 1, S0150: 1, H0539: 1, H0518: 1, S0152: 1, S0011: 1 and H0136: 1.			
246	HUSJN62	923146	256	1189 - 353	1156	Gly-14 to Glu-38, Asn-90 to Lys-100, Lys-150 to Val-158, Ser-166 to Gly-175. Gln-3 to Gly-9, Ala-100 to Phe-107, Lys-119 to Arg-130, His-132 to Leu-137, Glu-155 to Ser-167, Val-194 to Pro-204, Gly-225 to Ile-233.	AR089: 1, AR061: 0 H0617: 10, L0743: 4, S0358: 3, H0618: 3, H0052: 3, H0687: 3, H0135: 3, H0494: 3, L0646: 3, L0750: 3, L0731: 3, L0757: 3,	16		

L0601: 3, H0484: 2, H0662: 2, S0418: 2, H0549: 2, H0599: 2, H0150: 2, H0181: 2, H0087: 2, H0412: 2, H0529: 2, L0769: 2, L0649: 2, L0775: 2, L0663: 2, H0547: 2, L0742: 2, H0543: 2, H0556: 1, H0686: 1, H0685: 1, S0134: 1, S0218: 1, H0483: 1, H0661: 1, H0664: 1, S0360: 1, S0046: 1, S0278: 1, S0222: 1, H0441: 1, H0438: 1, H0592: 1, H0257: 1, H0486: 1, H0250: 1, H0042: 1, H0575: 1, H0253: 1, H0505: 1, H0318: 1, H0581: 1, H0545: 1, L0163: 1, S0051: 1, H0266: 1, S0338: 1, H0428: 1, H0039: 1, H0031: 1, H0606: 1, S0366: 1, S0036: 1, H0551: 1, H0059: 1, H0561: 1, H0647: 1, S0142: 1, H0538: 1, S0002: 1, S0426: 1, L0770: 1,							
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247	HTEIU92	1102681	257	1 - 564	1157	Asp-5 to Arg-13, Thr-37 to Ser-45, Ser-131 to Pro-137, Glu-154 to His-160, Lys-162 to Arg-168, Ile-180 to Asn-185.	AR061: 3, AR089: 1 H0038: 3	L0374: 1, L0771: 1, L0768: 1, L0774: 1, L0378: 1, L0776: 1, L0807: 1, L0512: 1, L0659: 1, L0666: 1, H0435: 1, H0672: 1, S0328: 1, S0152: 1, L0744: 1, L0751: 1, L0747: 1, L0749: 1, L0786: 1, L0755: 1, L0759: 1, S0434: 1, L0592: 1, L0604: 1, L0594: 1, L0595: 1, H0667: 1 and H0542: 1.		
		870652	796	1 - 339	1696	Asp-5 to Arg-13, Thr-37 to Ser-45.				
248	HAQMD86	1105267	258	1 - 1911	1158		AR061: 1, AR089: 1 L0748: 8, L0439: 8, L0766: 5, L0803: 5, L0749: 4, L0731: 4, S0046: 3, L0794: 3, L0805: 3, L0809: 3, L0666: 3, L0438: 3, H0543: 3, S0376: 2,			

S0007: 2, H0373: 2,
H0644: 2, L0455: 2,
L0598: 2, L0769: 2,
L0646: 2, L0804: 2,
L0774: 2, L0789: 2,
H0521: 2, H0627: 2,
L0743: 2, L0740: 2,
L0754: 2, L0595: 2,
H0170: 1, H0656: 1,
S0116: 1, H0638: 1,
H0125: 1, S0418: 1,
S0420: 1, S0356: 1,
S0360: 1, H0619: 1,
H0411: 1, H0586: 1,
H0486: 1, H0013: 1,
L0021: 1, H0098: 1,
H0575: 1, H0004: 1,
H0052: 1, S0228: 1,
H0266: 1, H0674: 1,
H0090: 1, H0063: 1,
H0641: 1, H0646: 1,
L0640: 1, L0763: 1,
L0770: 1, L0761: 1,
L0373: 1, L0800: 1,
L0641: 1, L0764: 1,
L0773: 1, L0783: 1,
H0144: 1, L0565: 1,
H0593: 1, H0659: 1,
H0658: 1, H0522: 1,
S0392: 1, L0751: 1,
L0747: 1, L0777: 1

249	HBJTG02	961459 1151462	797 259	2 - 1912 501 - 1418	1697 1159	Tyr-1 to Gly-6. Arg-12 to Tyr-23, Ser-93 to Thr-98, Lys-108 to Ser-113, Met-124 to Trp-129, Asp-173 to Ser-181, Pro-208 to Leu-213, Met-226 to Ser-231, Thr-250 to Pro-256, Glu-263 to Glu-273, Gln-301 to Arg-306.	AR089: 79, AR061: 26 L0002: 1, H0156: 1, L0021: 1, H0318: 1, H0561: 1, L0662: 1, L0794: 1, L0766: 1, S0026: 1, H0542: 1 and H0506: 1.			L0755: 1, L0757: 1, L0759: 1, S0026: 1, S0242: 1 and H0542: 1.
250	HBJUN65	919508 1151463	798 260	2 - 1087 2 - 532	1698 1160	Lys-49 to Thr-61, Ser-75 to Val-92, Phe-96 to Pro-124, Leu-139 to Ile-146. Lys-47 to Thr-59, Ser-73 to Val-90, Phe-94 to Pro-122, Leu-137 to Ile-144, Ile-197 to Trp-205, Glu-219 to Gly-228. Gly-7 to Tyr-15.	AR061: 8, AR089: 4 S0426: 2, S0126: 2, H0318: 1 and H0050: 1.			
251	HBMUI35	1195500	261	2117 - 288	1161		AR089: 8, AR061: 8 L0439: 13, L0438: 4, H0046: 3, L0663: 3, H0556: 2, H0023: 2, T0010: 2, L0769: 2.			

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812297	801	3 - 365	1701	<p>Ala-122 to Ser-132, Gly-151 to Arg-161, Glu-270 to Tyr-277, Cys-282 to Lys-290, Arg-402 to Glu-407, Gly-553 to Pro-561, Gly-615 to Gly-631, Pro-652 to Arg-660, Pro-662 to Ala-667, Pro-761 to Gly-768, Ser-792 to Ser-806.</p>	<p>H0550: 2, H0253: 2, S0002: 2, L0769: 2, L0783: 2, H0547: 2, H0555: 2, L0748: 2, L0747: 2, L0750: 2, L0758: 2, H0295: 1, S0114: 1, S0134: 1, H0255: 1, H0305: 1, S0420: 1, L0618: 1, S0376: 1, S0046: 1, H0619: 1, H0261: 1, S0222: 1, H0635: 1, T0082: 1, H0318: 1, L0040: 1, H0545: 1, H0201: 1, L0052: 1, H0688: 1, H0213: 1, H0031: 1, H0634: 1, H0087: 1, H0488: 1, H0561: 1, S0210: 1, L0639: 1, L0662: 1, L0768: 1, L0803: 1, L0655: 1, L0661: 1, L0658: 1, L0809: 1, L0666: 1, L0438: 1, H0539: 1, S0378: 1, H0518: 1, H0521: 1, L0741: 1, H0707: 1, L0584: 1, H0423: 1 and H0422: 1.</p>
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253	HFGMA55	1150870	263	1 - 444	1163	Phe-6 to Glu-15, Asp-21 to Leu-33, Met-141 to Cys-147.	AR061: 1, AR089: 1 L0439: 13, L0438: 4, H0046: 3, L0663: 3, H0556: 2, H0023: 2, T0010: 2, L0769: 2, L0655: 2, H0436: 2, L0743: 2, L0744: 2, L0748: 2, L0754: 2, L0747: 2, L0731: 2, L0759: 2, L0605: 2, S0116: 1, S0418: 1, H0619: 1, H0261: 1, S0222: 1, H0333: 1, H0492: 1, H0599: 1, H0052: 1, H0178: 1, H0050: 1, H0620: 1, H0179: 1, H0674: 1, S0364: 1, H0708: 1, H0100: 1, S0440: 1, S0142: 1, L0762: 1, L0796: 1, L0761: 1, L0521: 1, L0767: 1, L0766: 1, L0805: 1, L0652: 1, L0659: 1, L0783: 1, L0809: 1, L0665: 1, L0352: 1, H0660: 1, H0555: 1, L0749: 1, L0756: 1, L0777: 1, L0758: 1, L0595: 1 and H0542: 1.		
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254	HLHTE91	858681	802	3 - 416	1702	Thr-5 to Glu-13, Asp-19 to Leu-31.	AR050: 526, AR054: 486, AR051: 283, AR089: 1, AR061: 1 L0439: 5, L0662: 4, H0543: 4, L0766: 3, L0665: 3, L0751: 3, L0777: 3, H0618: 2, H0052: 2, H0024: 2, L0666: 2, H0265: 1, S0212: 1, H0580: 1, H0208: 1, H0393: 1, H0549: 1, H0550: 1, S0222: 1, H0333: 1, H0559: 1, H0486: 1, T0114: 1, S0049: 1, H0041: 1, H0083: 1, H0615: 1, L0055: 1, H0135: 1, H0038: 1, H0634: 1, H0616: 1, H0413: 1, L0370: 1, L0770: 1, L0800: 1, L0768: 1, L0794: 1, L0803: 1, L0804: 1, L0653: 1, L0658: 1, L0789: 1, H0520: 1, H0660: 1, S0044: 1, S0146: 1, L0743: 1, L0740: 1, L0749: 1
		789603	264	1 - 1203	1164		

						L0750: 1, L0779: 1, L0752: 1, L0755: 1, L0731: 1 and H0423: 1.		
						Glu-16 to Lys-21, Arg-30 to Pro-36, Ser-44 to Thr-49, Arg-136 to Arg-150, Leu-160 to Cys-173, Glu-223 to Gly-228, Gly-241 to Gln-249, Ala-260 to Gly-265, Ile-334 to Thr-349, Arg-364 to Glu-371.		
						Glu-9 to Ser-17, Phe-25 to Ala-34, Thr-43 to Asn-53, Met-172 to Gln-177.		

256	HNNBJ44	924193	805	2 - 625	1705	Glu-9 to Ser-17, Phe-25 to Ala-34, Thr-43 to Asn-53, Met-172 to Gln-177.	L0638: 1, L0761: 1, L0764: 1, L0662: 1, L0768: 1, L0774: 1, L0775: 1, L0518: 1, L0790: 1, H0520: 1, H0547: 1, H0365: 1, H0670: 1, H0666: 1, H0672: 1, L0756: 1, L0753: 1, L0757: 1, H0445: 1, S0026: 1, H0423: 1 and S0412: 1.	
		1151312	266	53 - 262	1166	Gln-9 to Lys-18, Gly-33 to Leu-64.	AR089: 1, AR061: 0 H0677: 2	
		915273	806	10 - 1665	1706	Arg-12 to Trp-26, Thr-28 to Glu-37, Leu-46 to Lys-51, Thr-85 to Glu-92, Arg-114 to Lys-119, Pro-191 to Asn-208, Lys-214 to Thr-224, Thr-242 to Asn-251, Ser-279 to Tyr-284, Leu-330 to Cys-344, Glu-364 to Tyr-369, Ile-375 to Met-384, Asn-413 to Ser-420.		

257	HSLJ146	997643	267	1 - 540	1167	Lys-457 to Pro-470, Gly-478 to Gln-483, Phe-519 to Cys-533.	Lys-1 to Gly-14, Gly-23 to Met-43, Ala-87 to Pro-99, Ile-101 to Ile-121, Gln-126 to Val-135, Val-139 to Cys-147.	AR089: 1, AR061: 0 H0521: 1 and S0390: 1.			
		883028	807	1 - 1551	1707		Lys-1 to Gly-14, Gly-23 to Ser-40.				
258	HTFOK70	1151518	268	1 - 609	1168	Ser-18 to Arg-25, Leu-45 to Pro-62, Gln-67 to Ala-72, Arg-143 to Gln-158, His-194 to Glu-203.		AR061: 0, AR089: 0 H0617: 2, L0589: 2, S0420: 1, S0046: 1, H0575: 1, H0251: 1, H0616: 1, L0775: 1, L0651: 1, L0665: 1, L0748: 1, L0754: 1, L0731: 1, L0758: 1 and S0424: 1.			
		914561	808	179 - 616	1708		Cys-10 to Lys-27, Arg-86 to Gln-101, His-137 to Glu-146.				
259	HUSXO71	1164014	269	3 - 317	1169	Ala-30 to Pro-36, Glu-59 to Thr-71, Ser-77 to Leu-90.		AR089: 14, AR061: 7 H0641: 4, L0596: 4, H0422: 4, L0768: 3, L0779: 3, L0758: 3, T0049: 2, H0486: 2, H0521: 2, H0522: 2, L0748: 2, L0747: 2,			

							L0777: 2, L0608: 2, L0601: 2, L0617: 1, H0497: 1, H0581: 1, H0544: 1, L0471: 1, H0687: 1, H0553: 1, H0090: 1, H0477: 1, H0413: 1, L0372: 1, L0774: 1, L0806: 1, L0659: 1, L0809: 1, L0789: 1, H0658: 1, H0648: 1, H0518: 1, L0750: 1, L0752: 1, L0731: 1, L0759: 1, L0590: 1 and H0423: 1.		
260	HWBDP39	1223498	809	648 - 1514	1709	Arg-1 to Gly-7, Leu-9 to Ser-16, Arg-25 to Cys-35.	AR089: 2, AR061: 1 L0439: 26, L0748: 22, L0744: 7, L0803: 6, L0805: 6, L0750: 6, H0013: 4, L0809: 4, L0766: 3, L0731: 3, L0758: 3, L0759: 3, H0624: 2, H0171: 2, H0156: 2, L0157: 2, L0471: 2, H0266: 2, H0059: 2, S0002: 2, H0529: 2, L0667: 2, L0800: 2, L0776: 2,		

261	HKMMQ73	810403	810	2 - 394	1710	Glu-19 to Gln-29, Arg-48 to Ser-53, Glu-57 to Lys-73.	AR051: 19, AR050: 9, AR054: 8 H0431: 1, H0096: 1, L0659: 1 and H0506: 1.	S0194: 1, H0542: 1, H0543: 1 and H0352: 1.		
262	HVV BK72	949559	811	66 - 257	1711	Ser-7 to Lys-29.	AR061: 1, AR089: 1 H0038: 1, H0672: 1 and L0758: 1.			
263	H7TXB52	981972	273	165 - 1322	1173	Glu-38 to Lys-43, Gly-125 to Thr-132.	AR089: 1, AR061: 0 L0731: 6, H0012: 5, L0803: 4, S0028: 4, H0497: 3, H0581: 3, H0561: 3, L0769: 3, S0418: 2, H0599: 2, L0770: 2, L0771: 2, S0266: 2, L0757: 2, L0591: 2, L0594: 2, L0362: 2, H0668: 2, H0542: 2, H0171: 1, S6024: 1, H0341: 1, H0483: 1, H0663: 1,			

							H0125: 1, S0045: 1, H0369: 1, T0039: 1, T0109: 1, H0250: 1, H0635: 1, H0620: 1, H0083: 1, H0266: 1, S0003: 1, H0628: 1, H0032: 1, H0100: 1, T0041: 1, L0641: 1, L0775: 1, L0776: 1, L0655: 1, L0606: 1, L0659: 1, L0809: 1, L0367: 1, L0789: 1, L0663: 1, H0144: 1, S0148: 1, H0519: 1, S0126: 1, H0478: 1, L0751: 1, L0750: 1, L0756: 1, L0759: 1, H0444: 1, S0196: 1 and H0543: 1.		
264	HDPY71	910910 1217205	813 274	165 - 1322 1365 - 661	1713 1174	Gly-92 to Pro-97, Cys-107 to Gln-131, Pro-139 to Ala-147, Pro-149 to Arg-160, Thr-194 to Pro-206.	AR050: 58, AR054: 53, AR051: 41, AR089: 1, AR061: 0 H0644: 2, H0265: 1, S0001: 1, S0358: 1, H0431: 1, T0039: 1, H0575: 1, S0010: 1, H0052: 1, H0263: 1, H0051: 1, H0416: 1, H0212: 1, L0796: 1		

									S0378: 1, H0521: 1, H0522: 1, S014: 1, S0027: 1 and L0747: 1.			
265	HGOCA12	971345	814	441 - 806	1714	Arg-85 to Lys-92, Leu-102 to Gln-115.			AR061: 210, AR089: 110 L0758: 3, S0364: 2, L0747: 2, S0278: 1, L0622: 1, H0018: 1, L0783: 1, L0809: 1, L0791: 1 and L0759: 1.			
266	HHCI29	971583	815	518 - 240	1715							
267	HODGC61	1077517	276	1 - 2073	1176							
		916885	816	2 - 574	1716							
		973449	277	43 - 324	1177	Thr-50 to Gln-57.			AR061: 8, AR089: 5 H0615: 3			
268	HBXGQ52	1229467	278	2 - 1003	1178	Gln-20 to Ser-28, Lys-31 to Arg-38, Asn-81 to His-93, Asn-148 to Asp-155, Met-182 to Gly-189, Pro-236 to Arg-243, Ala-258 to Ala-263, Pro-298 to Cys-304, Val-325 to Ala-333.			AR089: 4, AR061: 2 H0438: 3 and S0260: 1.			
269	HE2JS39	576093	817	1 - 291	1717							
		1121932	279	790 - 2	1179	Arg-1 to Lys-10, Gly-171 to Leu-176, Arg-217 to Arg-222,			AR089: 15, AR061: 10 L0750: 9, L0754: 5, L0779: 5, L0755: 4,			

						Glu-226 to Glu-232, Leu-257 to Ser-262.			L0360: 4, S0330: 3, L0747: 3, L0749: 2, L0777: 2, H0624: 1, H0650: 1, H0656: 1, S0376: 1, H0550: 1, H0592: 1, L0638: 1, H0689: 1, H0660: 1, L0731: 1, L0757: 1, L0759: 1 and L0359: 1.	
270	HE7SH21	957854 960302	818 280	51 - 716 3 - 1124	1718 1180	Gly-1 to Gly-6. Pro-11 to Ser-20, Ala-35 to Pro-41, Gln-88 to Trp-95, Arg-111 to Asp-119.			AR089: 1, AR061: 0 L0439: 5, L0592: 3, H0052: 2, L0438: 2, L0741: 2, L0747: 2, S0001: 1, L0005: 1, S0007: 1, H0101: 1, L0109: 1, H0009: 1, H0051: 1, L0769: 1, L0594: 1 and L0595: 1.	
271	HMI AO23	1103488	281	2 - 478	1181	Val-20 to Gln-36, Arg-67 to Gln-78, Pro-154 to Phe-159.			AR061: 4, AR089: 3 H0038: 2, L0439: 2, H0013: 1, S0010: 1, S6028: 1, H0090: 1, H0560: 1 and L0438: 1.	
272	HELDW45	944301	282	2 - 397 3 - 512	1719 1182	Asn-1 to Gln-9, Arg-40 to Glu-51. Arg-6 to Gln-13, Thr-44 to Ser-50, Pro-145 to Asn-168.			AR089: 820, AR061: 90 S0045: 1, S0278: 1, H0617: 1 and S0044: 1.	

273	HSRBB31	1121889	283	3 - 509	1183	Tyr-14 to Cys-23, Arg-41 to Lys-46, Ser-53 to Asp-74, Glu-106 to Gln-116, Ser-129 to Leu-135.	AR089: 8, AR061: 8 H0038: 3, S0418: 1, S0132: 1, H0261: 1, H0574: 1, H0046: 1, S0364: 1, S0011: 1 and S0192: 1.		
		958210	820	795 - 1676	1720				
274	HTEOW39	1151517	284	2 - 514	1184	Gly-40 to Val-46, His-66 to Ser-72, Trp-83 to Gly-88, Trp-143 to Gly-149.	AR089: 17, AR061: 14 H0616: 2		
		870566	821	2 - 445	1721	Gly-38 to Val-44.			
275	HE2PE32	1106571	285	1 - 468	1185	Ala-76 to Gly-82, Thr-98 to Leu-105, Glu-126 to Ala-132.	AR089: 0, AR061: 0 H0013: 3, H0271: 2 and H0171: 1.		
		524511	822	2 - 289	1722				
276	HSIDW39	1211446	286	2 - 748	1186		AR051: 12, AR054: 9, AR061: 5, AR089: 2, AR050: 0 H0036: 2, H0590: 2, S0354: 1, H0510: 1 and L0748: 1.		
		775139	823	1 - 501	1723				
		830774	824	12 - 419	1724	Glu-40 to Trp-57, Tyr-59 to Phe-64, Glu-91 to Arg-99, Asp-106 to Arg-114.			
277	HPMLD30	1226192	287	20 - 1666	1187	Val-22 to Asp-27, Gly-37 to Gln-42, Thr-48 to Glu-54,	AR089: 1, AR061: 0 H0624: 1, S0626: 1, S0278: 1, S0051: 1,		

278	HOEKP17	937414	1204712	825	6 - 521	1725	Lys-61 to Pro-68, Ser-80 to Ser-89, Asp-96 to Phe-101, Leu-146 to Asp-153, Asp-169 to Val-174, Lys-219 to Gly-234, Leu-241 to Gln-247, Asp-269 to Ala-278, Asn-281 to Trp-289.	H0416: 1, H0644: 1, S0052: 1, S0053: 1, S0028: 1, S0032: 1, S0031: 1 and S0260: 1.		
		937414	1204712	825	6 - 521	1725	Arg-12 to Arg-19, Trp-24 to Gly-35, Pro-42 to Arg-54, Ala-56 to Ser-61, Thr-78 to Asp-83, Thr-95 to Cys-108, Lys-174 to Lys-182, Lys-199 to Phe-210, Thr-222 to Ile-227.	AR061: 5, AR089: 2 L0754: 10, S0002: 3, L0766: 3, H0539: 3, H0370: 2, H0575: 2, H0581: 2, S0003: 2, H0038: 2, S0126: 2, L0751: 2, L0779: 2, L0758: 2, H0543: 2, H0664: 1, S0376: 1, H0639: 1, H0644: 1, L0055: 1, H0674: 1, H0090: 1, H0264: 1, H0561: 1, H0529: 1, L0640: 1, L0649: 1, L0803: 1, L0806: 1, H0684: 1, L0752: 1, L0753: 1, H0445: 1, L0608: 1 and L0362: 1.		
		931049		826	3 - 1055	1726	Arg-5 to Arg-12, Trp-17 to Gly-28,			

279	HFXDP67	1228141	289	198 - 1205	1189	Pro-35 to Arg-47, Ala-49 to Ser-54, Thr-71 to Asp-76, Thr-88 to Cys-101, Lys-167 to Lys-175, Lys-192 to Tyr-197. Pro-18 to Trp-24, Thr-32 to Asp-37, Arg-101 to Asp-107, Ala-148 to Ala-154, Gln-259 to Phe-264.	AR089: 0, AR061: 0 S0028: 4, S0126: 2, S0001: 1, S0282: 1, S0049: 1, S0050: 1, H0271: 1, H0388: 1 and S0390: 1.		
280	HJABA59	526951 1199933	827 290	266 - 616 2 - 904	1727 1190	Ala-21 to Ala-27. Pro-49 to Ala-59, Pro-127 to Phe-133, Arg-162 to Asn-173, Cys-183 to Asp-189, Lys-290 to Tyr-295.	AR061: 6, AR089: 3 L0755: 5, L0777: 4, L0752: 4, H0657: 3, S0016: 3, L0803: 3, S0330: 3, L0748: 3, L0740: 3, L0757: 3, H0622: 2, L0653: 2, L0666: 2, L0754: 2, L0779: 2, L0758: 2, S0040: 1, H0662: 1, L0481: 1, H0638: 1, S0418: 1, S0132: 1, H0393: 1, L0717: 1, H0586: 1, H0575: 1, H0052: 1, H0251: 1, L0157: 1, H0057: 1, S0003: 1, T0041: 1.		

281	HKIXB03	713642	828	366 - 902	1728	Arg-6 to Phe-11, Arg-40 to Asn-51, Cys-61 to Asp-67.	L0794: 1, L0766: 1, L0522: 1, L0659: 1, L0789: 1, L0664: 1, L0665: 1, H0144: 1, S0374: 1, H0648: 1, L0439: 1, L0780: 1, L0731: 1, L0759: 1, L0591: 1 and S0192: 1.		
		1129055	291	25 - 324	1191	Arg-1 to Val-10, Ala-36 to Gly-47, Leu-66 to Ser-79.	AR061: 5, AR089: 4 H0441: 2		
282	HKMMF49	924636	829	21 - 371	1729	Arg-1 to Val-10.	AR061: 4, AR089: 2 L0774: 4, L0803: 2, S0418: 1, S0360: 1, H0431: 1, L0157: 1, S0214: 1, H0551: 1, L0662: 1, L0767: 1, L0657: 1, L0659: 1, L0665: 1, H0660: 1 and L0777: 1.		
		1124742	292	1 - 600	1192	Gln-22 to Lys-28, Asp-69 to Leu-76, Phe-105 to Tyr-113, Leu-181 to Thr-190, Tyr-194 to Ser-200.			
283	HLD0G51	677960	830	1 - 600	1730	Gln-22 to Lys-28, Asp-69 to Leu-76, Phe-105 to Tyr-113.	AR089: 1, AR061: 0 H0090: 2, L0794: 2, L0605: 2, L0485: 2,		
		1151491	293	1 - 555	1193	Tyr-87 to Pro-92, Gln-119 to Ser-124, Glu-152 to Tyr-160.			

									S0354: 1, H0581: 1, H0052: 1, H0046: 1, H0510: 1, L0769: 1, L0363: 1, L0804: 1, L0755: 1, L0592: 1, S0242: 1 and H0422: 1.		
284	HSVAI25	918840	831	11 - 955	1731	Lys-46 to His-53, Tyr-135 to Pro-140, Gln-167 to Ser-172, Glu-200 to Tyr-208, Gln-298 to Pro-305.			AR089: 12, AR061: 9 L0752: 2, H0309: 1, L0518: 1 and S0152: 1.		
285	HSXCP56	577154 924635	832 295	99 - 245 213 - 962	1732 1195	Glu-1 to Pro-9, Val-48 to Gly-55, Pro-70 to Thr-79, Arg-94 to Arg-99, Arg-111 to Thr-121, Thr-146 to Arg-154, Thr-179 to Asp-185, Pro-194 to Ser-200, Pro-215 to Thr-220.			AR061: 7, AR089: 5 L0768: 3, L0439: 3, H0618: 2, H0253: 2, H0620: 2, H0616: 2, H0561: 2, L0764: 2, L0766: 2, L0653: 2, H0539: 2, L0744: 2, L0747: 2, L0750: 2, H0318: 1, H0123: 1, H0081: 1, S0051: 1, S0036: 1, H0038: 1, L0630: 1, L0772: 1, L0771: 1, L0794: 1, L0806: 1, L0809: 1, L0666: 1, L0438: 1,		

286	HBCAT08	1167275	296	47 - 2488	1196	H0682: 1, H0683: 1, L0756: 1, L0780: 1, L0752: 1, L0731: 1, L0758: 1 and L0759: 1. AR089: 1, AR061: 1 L0747: 24, L0591: 17, L0794: 15, L0777: 15, L0588: 10, L0750: 9, L0599: 9, S0046: 8, H0013: 8, H0619: 7, T0040: 7, L0748: 7, L0731: 7, L0665: 6, S3014: 6, S0212: 5, H0123: 5, L0471: 5, H0024: 5, L0754: 5, L0717: 4, H0333: 4, H0050: 4, H0286: 4, H0124: 4, L0770: 4, L0375: 4, H0144: 4, S0027: 4, L0749: 4, L0757: 4, L0759: 4, L0595: 4, H0170: 3, S0360: 3, H0208: 3, H0178: 3, H0012: 3, H0551: 3, H0100: 3, H0494: 3, L0763: 3, L0800: 3, L0641: 3, L0768: 3, L0766: 3, L0804: 3, L0659: 3, L0789: 3, S0126: 3		
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	S0037: 3, S0028: 3, L0740: 3, S0011: 3, H0624: 2, S0040: 2, H0295: 2, S0045: 2, H0645: 2, H0370: 2, H0427: 2, H0599: 2, H0544: 2, H0546: 2, H0594: 2, S0250: 2, H0428: 2, H0038: 2, H0623: 2, L0564: 2, S0210: 2, L0771: 2, L0662: 2, L0767: 2, L0776: 2, L0606: 2, L0783: 2, H0555: 2, L0741: 2, L0744: 2, L0605: 2, L0592: 2, L0593: 2, H0171: 1, T0049: 1, H0661: 1, S0420: 1, H0437: 1, S6022: 1, H0369: 1, H0550: 1, H0485: 1, H0486: 1, T0039: 1, L0021: 1, H0097: 1, H0309: 1, H0545: 1, H0009: 1, H0081: 1, H0620: 1, H0023: 1, H0057: 1, H0154: 1, H0014: 1, H0015: 1, H0083: 1, H0266: 1, H0188: 1, H0687: 1, H0288: 1, H0039: 1.	
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287	HHFBU53	920940	1048855	833	3 - 347	1733	Arg-19 to His-25.	H0622: 1, L0483: 1, H0644: 1, H0617: 1, H0673: 1, H0591: 1, H0087: 1, H0268: 1, H0269: 1, H0412: 1, H0056: 1, H0652: 1, L0769: 1, L0373: 1, L0764: 1, L0773: 1, L0521: 1, L0363: 1, L0649: 1, L0377: 1, L0388: 1, L0803: 1, L0775: 1, L0523: 1, L0806: 1, L0805: 1, L0653: 1, L0656: 1, L0558: 1, L0809: 1, L0647: 1, L0664: 1, L0565: 1, H0547: 1, H0435: 1, H0659: 1, H0670: 1, H0672: 1, S0380: 1, S0152: 1, H0704: 1, S3012: 1, S0206: 1, L0786: 1, L0758: 1, H0595: 1, L0589: 1, L0603: 1, H0665: 1, S0242: 1, S0276: 1, H0506: 1 and H0352: 1.	AR061: 4, AR089: 1 H0050: 1, L0748: 1,
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288	HTTDO45	837647	834	96 - 1061	1734	Ser-138 to Ser-144. Ala-1 to Thr-17, Ser-106 to Ser-112.	L0439: 1 and H0506: 1.		
		942505	298	327 - 1640	1198	Val-1 to Gly-10, Arg-24 to Asp-36, Leu-225 to Trp-231, Val-249 to Met-258, Glu-262 to Thr-269, Val-279 to Gly-284, Asp-307 to Asn-313, Arg-411 to Lys-416.	AR061: 10, AR089: 3 L0803: 24, S0358: 13, S0360: 7, L0774: 6, L0769: 5, L0794: 5, L0775: 5, L0777: 5, H0510: 4, L0439: 4, L0747: 4, L0731: 4, L0757: 4, L0601: 4, S0026: 4, H0556: 3, H0509: 3, L0662: 3, L0805: 3, L0776: 3, L0581: 3, L0608: 3, H0624: 2, T0002: 2, S0218: 2, S0354: 2, S0007: 2, H0333: 2, H0574: 2, H0599: 2, L0471: 2, H0373: 2, H0188: 2, H0644: 2, H0040: 2, L0761: 2, L0363: 2, L0766: 2, L0651: 2, L0659: 2, L0783: 2, L0789: 2, H0521: 2, S0028: 2, L0744: 2, L0748: 2, L0745: 2, L0749: 2, L0588: 2, L0362: 2, T0049: 1, H0657: 1,	18	

H0341: 1, H0638: 1, S0444: 1, H0637: 1, H0208: 1, H0441: 1, H0431: 1, H0586: 1, L0623: 1, H0013: 1, S0280: 1, H0575: 1, T0082: 1, H0581: 1, S0049: 1, L0033: 1, H0596: 1, L0040: 1, H0231: 1, S0362: 1, H0355: 1, H0622: 1, T0023: 1, S0366: 1, H0135: 1, H0163: 1, H0591: 1, H0551: 1, T0067: 1, H0059: 1, L0564: 1, S0142: 1, S0344: 1, L0764: 1, L0773: 1, L0768: 1, L0389: 1, L0804: 1, L0376: 1, L0527: 1, L0809: 1, L0665: 1, H0144: 1, H0547: 1, H0519: 1, S0126: 1, H0672: 1, S0330: 1, H0522: 1, H0134: 1, S0037: 1, L0754: 1, L0752: 1, L0755: 1, S0031: 1, H0707: 1, H0667: 1, H0542: 1, H0543: 1 and H0008: 1.

289	HTPII72	1104236	299	1 - 570	1199	Pro-21 to Asp-26, Asp-74 to Ser-83, Glu-104 to Asn-110, Gln-161 to Cys-167.	AR061: 10, AR089: 5 H0254: 1, H0255: 1, H0393: 1, H0333: 1, H0486: 1, N0009: 1, H0618: 1, H0622: 1 and H0625: 1.		
		958035	835	1 - 828	1735	Pro-21 to Asp-26, Asp-74 to Ser-83, Glu-104 to Asn-110, Gln-161 to Cys-167, Pro-189 to Pro-195.			
290	H6BSE22	1151371	300	147 - 662	1200	Met-4 to Lys-12, Gln-52 to Pro-72, Cys-80 to Gln-92, Thr-100 to Pro-105, Thr-149 to Asn-158, Leu-161 to Lys-172.	AR089: 1, AR061: 0 H0521: 4, L0766: 3, L0768: 2, S0152: 2, S0028: 2, S0308: 2, L0593: 2, S0212: 1, S0282: 1, H0662: 1, H0305: 1, S0358: 1, H0676: 1, H0580: 1, S0046: 1, H0586: 1, H0492: 1, H0013: 1, H0263: 1, H0046: 1, H0355: 1, H0416: 1, S0003: 1, H0591: 1, H0379: 1, T0042: 1, L0774: 1, L0784: 1, L0776: 1, L0789: 1, L0664: 1, H0701: 1, H0520: 1, H0547: 1, H0689: 1, H0690: 1,		

291	HDPAE43	1220621	301	3 - 1586	1201	Met-4 to Lys-12, Gln-52 to Pro-72, Cys-80 to Gln-92, Thr-100 to Pro-105, Thr-149 to Asn-158, Leu-161 to Asn-181, Ala-183 to Ser-191, Lys-295 to Leu-305, Glu-316 to Ser-322, Gly-330 to Met-353, Asp-393 to Tyr-426, Ser-435 to Ala-449, Lys-455 to Asn-463, Leu-466 to Tyr-477.	969019	836	147 - 1577	1736	L0749: 1, S0260: 1, H0668: 1 and H0665: 1.
						Ser-6 to Glu-13, Asp-35 to Leu-41, Ala-54 to Lys-62, Tyr-121 to Asp-126, Lys-132 to Ala-138, Phe-148 to Glu-157, His-163 to Thr-171, Ser-209 to Ser-220, Phe-234 to His-242, Tyr-261 to Ala-266, Arg-279 to Cys-296, Arg-370 to Glu-376, Ser-391 to Gln-398, Lys-420 to Ile-425,					AR089: 2, AR061: 0 L0794: 5, S0040: 4, H0052: 4, T0010: 4, H0560: 4, S0420: 3, L0455: 3, H0656: 2, S0212: 2, H0619: 2, H0497: 2, H0012: 2, H0429: 2, L0766: 2, H0520: 2, L0439: 2, H0665: 2, H0556: 1, H0650: 1, S0418: 1, H0580: 1, H0550: 1, H0370: 1, H0392: 1, H0333: 1, H0013: 1,

292	HDPFM16	1193042	837	2 - 472	1737	Ser-444 to Tyr-466, Gln-489 to Cys-497.	H0635: 1, H0505: 1, H0318: 1, H0581: 1, H0050: 1, H0373: 1, S025Q: 1, S0022: 1, H0553: 1, H0124: 1, L0370: 1, H0561: 1, H0593: 1, S0126: 1, H0435: 1, H0518: 1, H0521: 1, H0626: 1, L0748: 1, L0591: 1, H0542: 1, S0424: 1 and H0677: 1.		
		864998				Tyr-21 to Asp-26, Lys-32 to Ala-38, Phe-48 to Glu-57, His-63 to Thr-71.			
		1193042	302	596 - 1801	1202	Glu-1 to Gly-10, Arg-22 to Lys-27, Pro-99 to Asn-116, Lys-122 to Thr-132, Thr-150 to Asn-159, Ser-187 to Tyr-192, Leu-238 to Cys-252, Glu-272 to Tyr-277, Ile-283 to Met-292, Asp-321 to Ser-328, Lys-365 to Pro-378, Gly-386 to Gln-391.	AR089: 6, AR061: 2 H0457: 3, L0438: 3, L0748: 3, S0214: 2, H0038: 2, L0766: 2, L0731: 2, S0242: 2, H0677: 2, S0134: 1, S0346: 1, H0266: 1, H0644: 1, H0488: 1, S0210: 1, H0529: 1, L0800: 1, L0794: 1, H0521: 1, S3012: 1, L0439: 1, L0749: 1, L0750: 1 and H0423: 1.		
		810401	838	13 - 357	1738	Asp-10 to Lys-18.			

293	HFPCN10	1151478	303	81 - 548	1203	Ser-26 to Ser-34, Ser-43 to Lys-50. Ala-8 to Ser-23, Ser-68 to Gln-81.	AR061: 97, AR089: 57 H0556: 2, L0745: 2, H0542: 2, H0265: 1, S0222: 1 and L0471: 1.		
294	HLQFO35	915568 1161174	839 304	81 - 551 747 - 1037	1739 1204	Ala-8 to Ser-23, Ser-68 to Gln-81. His-32 to His-38.	AR061: 2, AR089: 1 S0412: 27, L0756: 3, H0644: 2, L0745: 2, H0574: 1, H0032: 1, L0598: 1, L0667: 1, L0766: 1, L0653: 1, L0749: 1, L0779: 1, L0759: 1 and S0026: 1.		
295	HMWU94	933901 1150834	840 305	80 - 184 105 - 572	1740 1205	Lys-75 to Asn-83, Leu-114 to Phe-121, Gln-145 to Lys-156.	AR061: 120, AR089: 64 H0341: 1, H0561: 1, L0790: 1 and L0777: 1.		
296	HSATQ28	705880 1124600	841 306	105 - 443 138 - 491	1741 1206	Pro-1 to Ser-8, Ser-10 to Ile-31, Ser-39 to Asp-48.	AR089: 120, AR061: 12 S0114: 2, H0422: 2 and L0748: 1.		
297	HTPIL46	866951 1196787	842 307	3 - 164 225 - 1898	1742 1207	Ser-14 to Thr-19, Thr-38 to Lys-44.	AR089: 12, AR061: 5 L0748: 14, H0457: 8, L0731: 5, L0770: 4,		

	H0521: 4, L0747: 4, H0543: 4, H0486: 3, H0591: 3, H0436: 3, L0777: 3, S0192: 3, H0542: 3, H0422: 3, S0046: 2, S0002: 2, L0667: 2, L0775: 2, L0655: 2, L0439: 2, L0749: 2, L0594: 2, H0170: 1, S0342: 1, S0114: 1, S0134: 1, S0001: 1, H0459: 1, S0222: 1, H0610: 1, H0013: 1, H0635: 1, H0575: 1, H0050: 1, H0271: 1, H0687: 1, S0214: 1, H0622: 1, L0483: 1, H0032: 1, H0038: 1, H0264: 1, H0560: 1, H0641: 1, H0647: 1, L0761: 1, L0771: 1, L0662: 1, L0766: 1, L0803: 1, L0650: 1, L0774: 1, L0805: 1, L0659: 1, L0789: 1, L0790: 1, H0699: 1, H0547: 1, S0152: 1, L0757: 1, H0445: 1, S0308: 1, L0601: 1, S0011: 1 and S0242: 1.	
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298	HNGEN37	973570	843	2 - 2218	1743	Gln-4 to Cys-9, Asp-23 to Pro-35, Leu-54 to Ile-59, Asn-61 to Asp-67, Val-93 to Lys-101, Gly-108 to Glu-136, Ser-145 to Thr-157, Thr-176 to Gln-186, Thr-194 to His-200, Lys-208 to Ser-215, Val-261 to Phe-267, Thr-297 to Arg-305, Lys-320 to Arg-327, Asn-336 to Asn-342, Glu-356 to Glu-365, Lys-375 to Tyr-385, Pro-407 to Val-413, Ser-417 to Leu-423, Thr-459 to Glu-467, Glu-503 to Val-508, Leu-564 to Cys-571, Glu-581 to Asp-590, Pro-611 to Val-621, Lys-625 to Gly-635, Asp-676 to Phe-684, Leu-709 to Cys-717.	AR089: 1, AR061: 0 S0052: 2			
		1103305	308	1 - 531	1208	Asn-10 to Arg-15, Asn-22 to Leu-27, Arg-90 to Lys-95.				
		663955	844	2 - 259	1744	Asn-9 to Arg-14,				

299	HLMDO77	974855	309	32 - 547	1209	Asn-21 to Leu-26.	AR061: 6, AR089: 6, AR051: 3, AR050: 2, AR054: 1			
		974856	845	403 - 215	1745	Gly-1 to Cys-9, Pro-12 to Pro-36.				
300	HNKAZ51	1154961	310	31 - 957	1210	Arg-11 to Arg-18, Gln-96 to Gln-102, Gln-121 to Gln-128, Gly-208 to Gln-216, Pro-231 to Ile-238.	AR050: 2, AR061: 1, AR089: 0, AR054: 0, AR051: 0 L0015: 1 and S0330: 1.			
		947067	846	31 - 612	1746	Arg-11 to Arg-18, Gln-96 to Gln-102, Gln-121 to Gln-128.				
301	HOGDR01	919899	311	3 - 977	1211	Cys-49 to Leu-55, Glu-62 to Glu-68, Phe-100 to Lys-106, Pro-122 to Gln-127, Leu-219 to Gly-225, Gly-273 to Gly-281.	AR054: 7, AR089: 2, AR061: 2, AR051: 1, AR050: 0 L0662: 3, L0653: 3, L0648: 2, L0659: 2, L0666: 2, H0435: 2, S0376: 1, H0550: 1, H0264: 1, S0472: 1, L0800: 1, L0643: 1, L0649: 1, L0803: 1, L0790: 1, H0672: 1, S0328: 1, L0779: 1 and S0260: 1.			
		947085	847	2 - 967	1747	Cys-46 to Leu-52, Glu-59 to Glu-65.				

302	HUKEP18	957456	312	852 - 265	1212		AR061: 14, AR054: 11, AR050: 9, AR089: 4 L0758: 2, H0059: 1, L0789: 1, L0665: 1, L0749: 1 and L0779: 1.		
303	HWHGF95	1155021	313	3 - 743	1213	Glu-25 to Trp-33, Trp-76 to Gln-83, Pro-94 to Asp-108.	AR050: 3, AR061: 2, AR054: 2, AR089: 1, AR051: 0 H0586: 1 and L0376: 1.		
		947019	848	2 - 742	1748	Glu-25 to Trp-33, Trp-76 to Gln-83, Pro-94 to Asp-108.			
304	HEMFC61	836514	314	1 - 714	1214	Glu-4 to Ser-9, Ser-58 to Arg-65.	AR061: 4, AR089: 3 H0038: 7, L0758: 5, H0616: 4, L0731: 4, S0002: 3, L0637: 3, H0623: 2, L0794: 2, L0809: 2, L0663: 2, H0522: 2, L0779: 2, L0777: 2, S0046: 1, H0431: 1, T0060: 1, H0013: 1, S0010: 1, H0545: 1, H0050: 1, S0023: 1, S0003: 1, H0328: 1, H0135: 1, H0163: 1, H0412: 1, H0102: 1, H0100: 1, T0042: 1, L0768: 1,		

									L0803: 1, L0375: 1, L0542: 1, L0647: 1, L0367: 1, L0791: 1, L0664: 1, H0693: 1, S0328: 1, S0168: 1, S0031: 1 and H0008: 1.			
305	HEOQP44	942596	315	157 - 1026	1215	Phe-62 to Arg-67, Gln-92 to Leu-104, Arg-163 to Leu-171, Ile-175 to Thr-182, Ser-237 to Ser-244, Ala-270 to Arg-277.			AR089: 1, AR061: 0 H0457: 2			
306	HHEKZ12	878267	316	9 - 395	1216	Phe-62 to Arg-67, Gln-92 to Leu-104.			AR089: 1, AR061: 0 H0542: 1			
307	HHELA35	878217	317	25 - 462	1217	Phe-62 to Arg-67, Gln-92 to Leu-104.			AR089: 1, AR061: 0 H0542: 1			
308	HSYBQ34	918789	318	96 - 1	1218				AR054: 22, AR050: 2, AR051: 1, AR089: 0, AR061: 0 H0624: 2, S0003: 2, H0519: 2, L0591: 2, H0171: 1, H0583: 1, S0418: 1, S0046: 1, H0619: 1, H0437: 1, H0497: 1, H0036: 1, H0590: 1, H0188: 1, H0039: 1, H0551: 1, H0623: 1, H0529: 1, H0520: 1, H0521: 1, H0522: 1, L0745: 1,			

								L0756: 1 and H0595: 1.		
309	HFCBA44	948533	849	2604 - 3473	1749		Phe-62 to Arg-67, Gln-92 to Leu-104.	AR089: 14, AR061: 9 H0457: 1, H0009: 1, L0666: 1, S0053: 1 and L0741: 1.		
310	HOUBE50	948519	320	1 - 243	1220		Ser-50 to Ser-66.	AR061: 1, AR089: 0 S0040: 1, S0222: 1, L0471: 1 and L0517: 1.		
311	HDPAS16	734057	321	1 - 495	1221		Glu-38 to His-43, Arg-58 to Thr-68.	AR089: 1, AR061: 0 L0803: 6, H0046: 4, L0666: 3, H0521: 3, L0731: 3, H0331: 2, H0574: 2, L0794: 2, L0774: 2, L0747: 2, H0686: 1, H0341: 1, H0545: 1, H0375: 1, H0687: 1, H0428: 1, L0455: 1, H0316: 1, S0036: 1, S0386: 1, S0002: 1, L0369: 1, L0642: 1, L0662: 1, L0364: 1, L0804: 1, L0776: 1, L0655: 1, L0659: 1, L0809: 1, L0663: 1, L0665: 1, H0670: 1, H0478: 1, L0749: 1, L0756: 1, L0752: 1, L0758: 1.		

									H0343: 1, L0608: 1, L0366: 1, S0192: 1, H0543: 1 and H0423: 1.			
312	HFLAA23	960332	322	2 - 784	1222				AR061: 106, AR089: 12 H0047: 2, H0181: 2 and S0260: 1.			
313	HCFMZ90	922112	323	273 - 881	1223			Asp-1 to Arg-8, Lys-15 to Asn-20, Thr-74 to Leu-80, Pro-84 to Asp-90.	AR061: 2, AR089: 1 L0749: 1, L0731: 1, L0757: 1 and H0423: 1.			
314	HFCES27	1103330	324	491 - 1120	1224			Thr-7 to Leu-13, Pro-17 to Asp-23, Ala-180 to Arg-188.	AR061: 1, AR089: 1 S0045: 2, L0646: 2, L0766: 2, L0776: 2, L0783: 2, L0731: 2, H0341: 1, H0663: 1, T0039: 1, L0021: 1, H0009: 1, T0042: 1, L0763: 1, L0764: 1, L0649: 1, L0775: 1, L0661: 1, S0328: 1, L0777: 1, L0757: 1, L0758: 1 and H0444: 1.			
315	HSDFK78	922115	850	372 - 1001	1750			Thr-7 to Leu-13, Pro-17 to Asp-23, Ala-180 to Arg-188.				
		1155464	325	1 - 306	1225			Tyr-5 to Thr-14, His-61 to Asn-70.	AR089: 6, AR061: 4 H0266: 1, H0416: 1 and S0031: 1.			
		582754	851	3 - 374	1751			Tyr-6 to Thr-13,				

316	HSDJX58	891067	326	729 - 1487	1226	His-60 to Asn-69. Tyr-101 to Glu-108, Pro-110 to Arg-116, Tyr-158 to Gln-164.	AR054: 11, AR050: 3, AR051: 3, AR089: 2, AR061: 2 L0748: 7, H0171: 2, H0624: 1, H0341: 1, S0280: 1, H0271: 1, H0032: 1, L0367: 1, L0439: 1, S0031: 1 and S0260: 1.		
317	HSLHV27	956591	852	786 - 7	1752	Tyr-101 to Glu-108, Pro-110 to Arg-116, Tyr-158 to Gln-164. His-8 to Gly-18.	AR050: 5, AR061: 2, AR054: 1, AR089: 1 S0028: 1		
318	HNGFU12	964075	853	983 - 21	1753	His-8 to Gly-18.	AR089: 4, AR061: 1 S0052: 1 and S0428: 1.		
319	HWLKA89	1105515	854	45 - 290	1754	Leu-59 to Gln-64.	AR089: 2, AR061: 0 S0358: 1, S0370: 1, L0803: 1, S0374: 1 and S0152: 1.		
320	HLWBU48	735158	855	1 - 318	1755	Lys-1 to Ile-6, Pro-28 to Glu-37, Leu-58 to Arg-65, Pro-95 to Glu-102, Arg-104 to Gly-111,	AR089: 8, AR061: 5 L0754: 3, H0553: 2, L0731: 2, L0005: 1, H0581: 1, H0271: 1, H0644: 1 and H0521: 1.		

321	HWWEY71	1204720	721520	856	2 - 280	1756	<p>Glu-118 to Glu-123, Glu-125 to Ala-130, Gly-142 to Gly-151. Ile-5 to Pro-10, Lys-36 to Thr-41. Pro-17 to His-24, Pro-26 to Asp-33, Pro-66 to Lys-72, Thr-149 to Arg-158, Asp-172 to Glu-178, Ala-279 to Ser-289, Arg-306 to Arg-314, Val-330 to Lys-336, Asp-347 to Arg-353, Arg-358 to Gln-363.</p>	<p>AR089: 1, AR061: 0 H0556: 24, H0521: 12, H0551: 9, H0265: 8, H0692: 8, H0543: 8, S0418: 7, L0748: 7, H0542: 7, H0318: 6, H0560: 6, S0314: 6, H0445: 6, L0665: 5, L0747: 5, H0423: 5, H0341: 4, H0617: 4, L0769: 4, L0439: 4, L0740: 4, L0750: 4, L0595: 4, S0278: 3, H0052: 3, H0622: 3, H0135: 3, H0040: 3, S0144: 3, L0768: 3, L0766: 3, L0775: 3, L0776: 3, H0547: 3, S0328: 3, S0206: 3, L0591: 3, L0608: 3, H0422: 3, H0170: 2, H0657: 2, H0484: 2, S0045: 2, S0046: 2, H0545: 2, H0050: 2, H0012: 2, H0620: 2</p>		
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H0083: 2, H0284: 2, H0087: 2, H0488: 2, L0640: 2, L0771: 2, L0773: 2, L0521: 2, L0363: 2, L0783: 2, L0383: 2, L0663: 2, L0438: 2, H0520: 2, L0751: 2, L0731: 2, L0757: 2, L0596: 2, L0362: 2, T0002: 1, H0686: 1, S0040: 1, S0218: 1, H0583: 1, H0656: 1, S0180: 1, S0212: 1, H0483: 1, H0177: 1, H0125: 1, S0420: 1, S0356: 1, S0376: 1, S0360: 1, S0408: 1, H0208: 1, S0132: 1, H0619: 1, H0393: 1, L0717: 1, H0586: 1, H0587: 1, H0642: 1, H0331: 1, H0256: 1, T0109: 1, H0013: 1, H0599: 1, T0082: 1, S0182: 1, H0309: 1, T0110: 1, H0327: 1, H0544: 1, H0041: 1, S0051: 1, H0266: 1, H0290: 1, H0252: 1, H0328: 1, H0604: 1, H0031: 1.

									L0601: 1, S0011: 1, H0668: 1, S0192: 1, S0276: 1 and S0424: 1.		
322	HHFGD45	970546	857	71 - 775	1757	Ala-46 to Pro-68, Gln-75 to Gly-84, Leu-106 to Gly-121, Pro-208 to Lys-214.			AR061: 2, AR089: 1 S0053: 2, S0045: 1, H0619: 1, H0318: 1 and H0050: 1.		
323	HNHEB44	584855 1161293	858 333	1 - 267 643 - 2	1758 1233	Phe-3 to Cys-8, Ser-64 to Gln-69.			AR061: 1, AR089: 0 S0053: 2, S0045: 1, H0619: 1, H0318: 1 and H0050: 1.		
324	HMACX92	683284 1151497	859 334	1 - 195 119 - 1138	1759 1234	His-27 to Thr-32. Glu-140 to Trp-147, Asn-323 to Glu-329.			AR061: 5, AR089: 2 S0144: 4, L0803: 2, H0682: 2, H0521: 2, H0295: 1, L0005: 1, H0645: 1, H0549: 1, T0060: 1, H0327: 1, H0545: 1, H0050: 1, H0012: 1, H0620: 1, H0510: 1, H0687: 1, H0617: 1, H0059: 1, H0509: 1, H0641: 1, S0002: 1, L0646: 1, L0374: 1, L0794: 1,		

									L0804: 1, L0775: 1, L0656: 1, L0809: 1, L0790: 1, L0664: 1, S0052: 1, H0520: 1, L0749: 1, H0653: 1 and S0194: 1.		
325	HNTBW57		922250	860	140 - 1159	1760			AR089: 0, AR061: 0 L0794: 4, H0435: 2, H0632: 1, H0013: 1, H0030: 1, S0150: 1, L0649: 1, H0547: 1, H0519: 1, H0689: 1, L0759: 1 and H0677: 1.		
326	HBSDC13		1193070	335	1 - 1263	1235		Pro-1 to Gly-18, Arg-29 to Pro-42, Glu-80 to Arg-86, Gly-239 to Pro-247, Pro-410 to Thr-419.			
			867327	861	2 - 682	1761			AR089: 8, AR061: 4 H0305: 4, H0419: 1 and S0045: 1.		
327	HCWBX21		657402	862	3 - 233	1762			AR061: 1, AR089: 0 H0305: 4, H0419: 1 and S0045: 1.		
			920486	337	49 - 333	1237		Glu-52 to Gly-57, Cys-69 to Asp-83, Lys-88 to Met-93.			
328	HFRBW72		916944	338	365 - 679	1238		Arg-10 to Lys-16.	AR061: 3, AR089: 1 S0028: 5, S0126: 2, S0001: 1, S0282: 1, S0045: 1, S0049: 1, S0050: 1, H0271: 1, H0388: 1, S0390: 1, S0260: 1 and H0008: 1.		
329	HSLJX23		1105530	339	2 - 496	1239		Met-12 to Gly-17.	AR089: 1, AR061: 0		

330	HSLJX90	837470 1105297	863 340	2 - 256 1 - 438	1763 1240	Glu-29 to Asp-35, Glu-113 to Leu-120, Ala-123 to Gly-133, Ala-138 to Lys-143. Arg-21 to Glu-27.	S0390: 1 and S0031: 1. AR089: 1, AR061: 0 H0150: 1, S0390: 1 and S0027: 1.		
331	HAUAI67	787575 1102604	864 341	2 - 358 107 - 727	1764 1241	Arg-13 to Arg-19, Asp-37 to Asp-43, Glu-127 to Asp-132, Asn-152 to Glu-171, Ala-179 to Ala-193.	AR061: 4, AR089: 2 L0748: 18, L0749: 8, L0755: 7, H0686: 4, S0360: 3, H0519: 3, H0659: 3, L0747: 3, L0758: 3, H0341: 2, H0622: 2, H0040: 2, H0616: 2, L0772: 2, L0375: 2, L0754: 2, L0779: 2, H0542: 2, H0294: 1, H0657: 1, H0656: 1, S0116: 1, H0663: 1, H0638: 1, S0376: 1, H0393: 1, H0083: 1, H0030: 1, L0055: 1, H0068: 1, H0591: 1, H0038: 1, H0412: 1, H0100: 1, L0475: 1, S0422: 1, L0763: 1, L0771: 1, L0767: 1, L0768: 1, L0784: 1, L0776: 1, L0633: 1, L0783: 1,		

332	HDPTA89	929241 953718	865 342	230 - 652 20 - 433	1765 1242	Gly-22 to Phe-27, Tyr-36 to Ala-48, Glu-51 to Pro-79, Pro-102 to His-113.	AR089: 1, AR061: 1 L0777: 13, L0751: 10, L0769: 7, L0766: 6, L0758: 6, H0618: 4, H0617: 4, L0771: 4, L0776: 4, L0757: 4, L0759: 4, H0494: 3, L0761: 3, H0521: 3, L0754: 3, H0265: 2, H0650: 2, S0045: 2, H0427: 2, H0253: 2, H0318: 2, H0150: 2, L0794: 2, L0805: 2, L0665: 2, L0743: 2, L0439: 2, L0749: 2, L0750: 2, L0752: 2, H0445: 2, H0556: 1, S0342: 1, S0218: 1, L0785: 1, H0484: 1, L0481: 1, S0418: 1, S0420: 1, H0637: 1, H0549: 1, H0587: 1, H0333: 1 H0486: 1	L0665: 1, H0144: 1, H0682: 1, S0378: 1, H0627: 1, L0752: 1, L0731: 1, S0026: 1, H0665: 1, S0242: 1 and H0543: 1.		
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333	HMCBN45	927125	343	3 - 686	1243	Lys-50 to Gly-56, Pro-114 to Gly-122, Glu-129 to Tyr-134, Ala-174 to Leu-179, Arg-210 to Tyr-222.	S0280: 1, H0599: 1, S0346: 1, H0194: 1, T0115: 1, H0597: 1, H0231: 1, H0046: 1, H0083: 1, H0266: 1, H0188: 1, H0688: 1, H0424: 1, H0213: 1, H0181: 1, S0364: 1, H0616: 1, H0087: 1, H0551: 1, H0412: 1, H0623: 1, H0100: 1, T0041: 1, S0150: 1, H0695: 1, L0796: 1, L0643: 1, L0662: 1, L0803: 1, L0775: 1, L0809: 1, L0789: 1, L0663: 1, L0664: 1, H0691: 1, S0126: 1, H0682: 1, S0152: 1, H0555: 1, H0627: 1, S0027: 1, L0779: 1, L0780: 1, L0753: 1, L0596: 1, H0668: 1, H0667: 1 and H0543: 1.	AR089: 9, AR061: 8 T0042: 2, H0556: 1, H0486: 1, L0586: 1, H0083: 1, H0641: 1, S0142: 1, H0529: 1 and H0435: 1
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334	HTTJY18	1223495	344	352 - 1281	1244	Ala-7 to His-20, Arg-38 to Gly-48, His-89 to Trp-98, Thr-125 to Arg-130, Ala-133 to Cys-140, Ser-157 to Leu-171, Asp-201 to Ile-206, Gln-231 to Lys-238, Thr-240 to Thr-259, Gly-266 to Gly-277.	AR089: 1, AR061: 0 L0766: 50, L0754: 12, L0740: 11, S0358: 9, L0803: 8, H0575: 7, L0731: 7, L0747: 6, L0761: 5, L0662: 5, L0805: 5, L0744: 5, L0748: 5, L0779: 5, L0794: 4, L0749: 4, L0750: 4, L0752: 4, L0757: 4, L0362: 4, L0471: 3, S0210: 3, L0806: 3, H0144: 3, S0126: 3, S0328: 3, L0743: 3, L0777: 3, L0759: 3, H0423: 3, S0376: 2, H0013: 2, S0474: 2, H0581: 2, H0179: 2, H0628: 2, H0038: 2, H0264: 2, H0623: 2, H0641: 2, S0142: 2, S0426: 2, L0800: 2, L0771: 2, L0768: 2, L0649: 2, L0774: 2, L0655: 2, L0607: 2, L0791: 2, S0374: 2, L0438: 2, H0436: 2, L0745: 2, L0746: 2, L0756: 2, L0753: 2, L0755: 2, S0026: 2, H0170: 1,		
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	S0114: 1, H0341: 1, S0001: 1, H0664: 1, H0638: 1, S0442: 1, S0046: 1, S6022: 1, H0611: 1, H0370: 1, H0642: 1, L0021: 1, H0599: 1, H0003: 1, L0022: 1, H0036: 1, H0004: 1, H0274: 1, S0010: 1, L0105: 1, H0421: 1, H0052: 1, H0251: 1, H0596: 1, H0046: 1, H0572: 1, H0050: 1, H0242: 1, H0012: 1, S0050: 1, H0014: 1, H0083: 1, H0375: 1, S0250: 1, S0003: 1, T0023: 1, L0483: 1, T0006: 1, H0031: 1, L0142: 1, L0055: 1, H0032: 1, H0674: 1, L0455: 1, S0036: 1, H0135: 1, H0090: 1, H0040: 1, H0634: 1, H0616: 1, T0067: 1, H0488: 1, H0433: 1, H0413: 1, H0056: 1, H0560: 1, L0598: 1, H0529: 1, L0369: 1, L0762: 1, L0770: 1, L0638: 1,	
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									L0373: 1, L0372: 1, L0764: 1, L0773: 1, L0804: 1, L0776: 1, L0659: 1, L0518: 1, L0384: 1, L0789: 1, L0790: 1, L0666: 1, L0663: 1, L0664: 1, S0148: 1, H0547: 1, H0659: 1, H0670: 1, H0539: 1, S0378: 1, H0518: 1, H0521: 1, H0696: 1, H0555: 1, H0478: 1, S0028: 1, L0758: 1, H0445: 1, L0588: 1, S0192: 1, H0543: 1, S0458: 1 and S0384: 1.		
335	HMAJL09	950989	866	238 - 1263	1766	Asp-1 to Pro-17.	AR089: 0, AR061: 0 S0278: 1				
		1157337	345	68 - 526	1245	Tyr-22 to Arg-30, Arg-77 to Gly-83.					
		950168	867	2 - 493	1767	Tyr-30 to Ser-35, Arg-94 to Gly-100.					
336	HSVCH37	558195	346	3 - 122	1246		AR089: 1, AR061: 1 H0309: 2	4q25-q27	137600, 147680, 189800, 217030, 248510, 600919, 601542		
337	HTOCG37	708888	347	3 - 218	1247	Asn-7 to Thr-18.	AR061: 11, AR089: 6				

338	HBXAW47	771624	348	243 - 656	1248	His-8 to Arg-13, Ser-23 to Lys-30.	Glu-34 to Ser-39, His-59 to Asn-64.	L0777: 4, L0766: 3, L0776: 3, L0439: 3, H0031: 2, L0809: 2, H0694: 2, L0591: 2, S6024: 1, H0656: 1, H0369: 1, H0051: 1, T0067: 1, H0272: 1, L0769: 1, L0805: 1, L0518: 1, L0519: 1, H0684: 1, L0779: 1, S0031: 1, L0584: 1 and L0366: 1.		
								AR089: 5, AR061: 1 L0748: 5, L0438: 3, L0747: 3, L0731: 3, L0005: 2, S0360: 2, L0769: 2, L0794: 2, L0766: 2, L0803: 2, L0655: 2, L0756: 2, L0758: 2, S0356: 1, L0717: 1, H0033: 1, H0617: 1, H0413: 1, S0038: 1, S0422: 1, S0426: 1, L0639: 1, L0646: 1, L0662: 1, L0378: 1, L0636: 1, L0647: 1, L0367: 1, L0789: 1, L0666: 1, H0436: 1, L0779: 1, L0777: 1, L0752: 1.		

339	HBXAW27	909801	349	1111 - 1830	1249	Gly-19 to Cys-25, Pro-56 to Phe-68, Gly-94 to Pro-99, Lys-113 to Leu-119, Pro-126 to Gln-131, Lys-138 to Leu-145.	L0753: 1, L0608: 1 and L0601: 1. AR089: 2, AR061: 1 L0741: 10, H0052: 6, S0036: 3, L0439: 3, S0388: 2, L0770: 2, L0438: 2, S0300: 1, S0222: 1, H0441: 1, L0021: 1, S0010: 1, S0049: 1, H0327: 1, H0150: 1, H0009: 1, H0569: 1, H0051: 1, S0051: 1, T0010: 1, L0456: 1, S0038: 1, H0100: 1, L0370: 1, L0517: 1, L0742: 1, L0745: 1, L0592: 1 and L0366: 1.	12q13	107777, 123940, 139350, 139350, 148040, 148041, 148043, 148070, 231550, 600194, 600231, 600536, 600808, 600956, 601284, 601769, 601769, 601928, 602116, 602153
340	HSLJE54	926924	350	3 - 731	1250	Arg-1 to Gly-7, Pro-25 to His-34, Leu-36 to Lys-49.	AR061: 0, AR089: 0 S0036: 1, H0521: 1, H0436: 1 and S0390: 1.		
341	HBXBG65	932780	351	2 - 535	1251	Asn-1 to Arg-10, Pro-105 to Val-114, Gln-130 to Glu-140.	AR089: 1, AR061: 0 H0144: 2, S0038: 1 and L0439: 1.	14q32.1	107280, 107280, 107400, 107400, 122500,

									186960, 245200, 601841
342	HE8CG83	933609	352	703 - 1128	1252			AR089: 17, AR061: 8 L0748: 3, H0650: 1, S0007: 1, H0013: 1, H0618: 1, H0051: 1, S0051: 1, H0553: 1, H0268: 1 and S0031: 1.	
343	HOGCW55	953161	353	90 - 392	1253			AR061: 1, AR089: 1 H0620: 3 and H0435: 1.	
344	HNTND64	954871	354	1 - 264	1254	Gln-34 to Glu-42.		AR089: 8, AR061: 5 S0040: 1, H0083: 1 and H0520: 1.	
345	HHAWC08	957942	355	172 - 1047	1255	Pro-14 to Gly-32, Pro-73 to Glu-83, Phe-92 to Ser-100, Glu-141 to Asp-148, Thr-159 to Gln-166, Asp-198 to Pro-204, Thr-242 to Val-248.		AR061: 0, AR089: 0 H0052: 2, L0439: 2, S0418: 1, H0619: 1, S0280: 1 and L0438: 1.	
346	HFPEN04	964824	356	88 - 540	1256	Glu-62 to Tyr-67, Ser-129 to Asp-135.		AR061: 5, AR089: 2 S0010: 4, S0222: 3, H0455: 2, L0803: 2, L0439: 2, L0745: 2, S0282: 1, S0400: 1, H0456: 1, H0441: 1, S0346: 1, H0509: 1, L0769: 1, L0438: 1,	

347	HTZMB51	496523	357	58 - 399	1257	Cys-1 to Asp-10, Thr-16 to Asn-22.	L0756: 1 and S0106: 1. AR089: 1, AR061: 1 S0045: 1, H0623: 1 and S3020: 1.		
348	HNHDK43	529500	358	1 - 396	1258	Thr-7 to Gly-13.	S0053: 1 and S0037: 1.		
349	HTTDP32	558751	359	1 - 360	1259	Asn-21 to Asn-31.	AR061: 4, AR089: 3 L0789: 2, H0069: 1, H0052: 1, H0266: 1, H0040: 1, S0210: 1 and H0519: 1.	116806, 120120, 120120, 120120, 120120, 120436, 120436, 120436, 138320, 168468, 182280, 190182, 190182, 227646, 261510, 600163, 601154	3p22-p21.3
350	HSLFP27	572920	360	478 - 2	1260	Phe-44 to Arg-49.	AR089: 1, AR061: 0 S0126: 4, S0028: 2 and S0031: 2.		
351	HMTAL73	621705	361	73 - 450	1261	Val-99 to Gly-106.	AR089: 2, AR061: 2 H0518: 1 and L0362: 1.	192340, 234200	20p13
352	HMHQBQ53	715301	362	404 - 201	1262	Asp-22 to Gly-34, Lys-37 to Glu-42.	AR089: 39, AR061: 13 L0745: 8, L0740: 6, L0747: 5, L0794: 4,		

	L0666: 4, S0360: 3, H0150: 3, H0031: 3, H0617: 3, L0769: 3, H0662: 2, S0182: 2, H0286: 2, H0135: 2, L0770: 2, L0662: 2, L0803: 2, H0547: 2, L0743: 2, L0752: 2, L0753: 2, L0731: 2, L0758: 2, L0593: 2, H0556: 1, S0342: 1, H0341: 1, S0212: 1, H0671: 1, S0418: 1, S0420: 1, S0358: 1, H0392: 1, H0587: 1, H0575: 1, H0253: 1, H0318: 1, H0052: 1, H0545: 1, H0046: 1, H0050: 1, H0408: 1, H0510: 1, H0375: 1, H0099: 1, H0247: 1, H0687: 1, H0628: 1, H0551: 1, H0509: 1, S0344: 1, S0210: 1, L0761: 1, L0772: 1, L0646: 1, L0643: 1, L0764: 1, L0364: 1, L0774: 1, L0653: 1, L0655: 1, L0636: 1, L0783: 1, L0809: 1, H0144: 1, L0438: 1,	
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							H0593: 1, S0330: 1, H0518: 1, L0748: 1, L0439: 1, L0751: 1, L0754: 1, L0749: 1, L0757: 1, L0759: 1, H0653: 1, H0542: 1 and H0423: 1.			
353	HBICG44	715860	363	377 - 138	1263		AR061: 22, AR089: 5 18 L0803: 23, S0360: 7, S0358: 6, L0794: 5, L0777: 5, H0510: 4, L0439: 4, L0731: 4, L0757: 4, S0026: 4, H0509: 3, L0662: 3, L0805: 3, L0608: 3, H0624: 2, T0002: 2, S0218: 2, S0007: 2, H0333: 2, H0574: 2, L0471: 2, H0373: 2, H0188: 2, H0644: 2, L0363: 2, L0766: 2, L0774: 2, L0651: 2, L0776: 2, L0659: 2, L0789: 2, H0521: 2, L0748: 2, L0745: 2, L0747: 2, L0749: 2, L0581: 2, L0362: 2, L0601: 2, H0556: 1, T0049: 1, H0657: 1, H0638: 1, S0354: 1			

354	HSKXN70	753717	364	3 - 356	1264	Glu-30 to Glu-38, Asn-47 to Tyr-58.	AR089: 1, AR061: 1 L0439: 4, L0770: 2, L0794: 2, L0438: 2, L0740: 2, H0599: 1, T0082: 1, S0003: 1, H0644: 1, L0639: 1	S0444: 1, H0637: 1, H0208: 1, H0441: 1, H0431: 1, H0586: 1, L0623: 1, S0280: 1, H0575: 1, T0082: 1, H0581: 1, S0049: 1, L0033: 1, H0596: 1, L0040: 1, H0231: 1, H0355: 1, H0622: 1, T0023: 1, S0366: 1, H0163: 1, H0040: 1, H0551: 1, T0067: 1, L0564: 1, L0764: 1, L0389: 1, L0804: 1, L0775: 1, L0376: 1, L0527: 1, L0783: 1, L0809: 1, L0665: 1, H0144: 1, H0672: 1, S0330: 1, H0522: 1, H0134: 1, S0028: 1, L0744: 1, L0754: 1, L0755: 1, S0031: 1, L0588: 1, H0543: 1 and H0008: 1.	
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								S3014: 1, S0028: 1, S0206: 1, L0756: 1, L0779: 1 and L0752: 1.			
355	HPAC32	815942	365	3 - 371	1265			AR089: 1, AR061: 0 S0028: 2, H0624: 1, S0278: 1, S0150: 1 and H0689: 1.			
356	HHPFP57	835955	366	128 - 688	1266			AR061: 4, AR089: 4			
357	HFKJW01	836491	367	3 - 440	1267			AR089: 1, AR061: 0 H0620: 2, H0012: 1, S0152: 1 and S0260: 1.			
358	HSDFL63	836498	368	1 - 249	1268		Glu-1 to Asp-7, Met-53 to Met-60, Phe-78 to Ser-83.	AR061: 402, AR089: 142 H0038: 7, L0758: 5, H0616: 4, L0731: 4, S0002: 3, L0637: 3, H0623: 2, L0794: 2, L0809: 2, L0663: 2, H0522: 2, L0779: 2, L0777: 2, S0046: 1, H0431: 1, T0060: 1, H0013: 1, S0010: 1, H0545: 1, H0050: 1, S0023: 1, S0003: 1, H0328: 1, H0135: 1, H0163: 1, H0412: 1, H0102: 1, H0100: 1, T0042: 1, L0768: 1, L0803: 1, L0375: 1,			

								L0542: 1, L0647: 1, L0367: 1, L0791: 1, L0664: 1, H0693: 1, S0328: 1, S0168: 1, S0031: 1 and H0008: 1.			
359	HLD0008	857070	369	3 - 449	1269	Phe-13 to Lys-19, Gln-21 to Ser-37, Arg-44 to Tyr-60, Cys-84 to Asn-89, Thr-122 to Thr-128.		AR089: 3, AR061: 3 H0333: 1 and H0510: 1.			
360	HMSHN43	867363	370	49 - 375	1270	Pro-16 to Arg-23.		AR061: 7, AR089: 4 S0354: 2, S0212: 1, H0484: 1, H0402: 1, S0358: 1, H0457: 1, H0213: 1, H0634: 1, H0059: 1, H0494: 1, S0002: 1, L0648: 1, L0438: 1, H0521: 1 and L0751: 1.			
361	HBXCT92	871044	371	3 - 1451	1271	Pro-18 to Trp-25, Arg-164 to Ser-169, Pro-174 to Gln-185, Lys-220 to Phe-226, Ser-272 to Lys-290, Cys-316 to Val-329, Glu-431 to Gln-436, Ile-463 to Val-470.		AR089: 1, AR061: 1 H0544: 4, L0438: 4, L0439: 3, L0747: 3, S0036: 2, L0794: 2, H0539: 2, L0748: 2, L0485: 2, S0424: 2, S0116: 1, S0360: 1, S0046: 1, H0411: 1, H0261: 1, H0455: 1, H0574: 1, H0632: 1, L0021: 1, H0575: 1,			

									H0618: 1, H0052: 1, H0251: 1, H0309: 1, H0327: 1, S0050: 1, S0628: 1, L0456: 1, S0038: 1, H0494: 1, L0520: 1, L0764: 1, L0375: 1, L0657: 1, L0528: 1, H0660: 1, S0044: 1, S0028: 1, L0758: 1, L0759: 1, L0596: 1, L0592: 1, S0011: 1 and S0192: 1. AR061: 6, AR089: 2		
362	H6EDP44	875744	372	157 - 876	1272				AR089: 4, AR061: 4 H0265: 3, H0592: 2, H0494: 2, L0761: 2, L0374: 2, L0804: 2, H0519: 2, H0593: 2, H0556: 1, H0657: 1, H0656: 1, H0662: 1, S0358: 1, S0376: 1, H0437: 1, H0253: 1, H0375: 1, H0059: 1, L0646: 1, L0768: 1, L0766: 1, L0803: 1, L0774: 1, L0775: 1, L0658: 1, L0809: 1, L0666: 1, H0520: 1, H0539: 1, S0027: 1 and		
363	HLJBF94	875745	373	153 - 668	1273	Arg-1 to Trp-9, Ala-25 to Ser-30.					

364	HTEHO28	877182	374	1286 - 438	1274	Ser-14 to Gln-19.	H0543: 1. AR061: 7, AR089: 4 T0039: 1, H0123: 1, H0038: 1, H0040: 1, T0042: 1, S0126: 1, H0631: 1, L0596: 1 and H0506: 1.		
365	HE9PC30	880696	375	1 - 390	1275	Arg-2 to Lys-28, Lys-43 to His-48, Arg-66 to Gly-76, His-117 to Cys-130.	AR089: 2, AR061: 2 L0766: 17, H0038: 2, L0794: 2, L0803: 2, H0144: 2, L0362: 2, S0114: 1, H0013: 1, H0575: 1, H0596: 1, H0046: 1, L0471: 1, S0250: 1, L0142: 1, H0628: 1, H0032: 1, H0135: 1, H0634: 1, H0616: 1, H0413: 1, H0056: 1, S0142: 1, L0598: 1, L0774: 1, L0789: 1, L0790: 1, L0791: 1, S0126: 1, H0478: 1, S0028: 1, L0743: 1, L0744: 1, L0754: 1, L0745: 1, L0746: 1, L0747: 1, L0750: 1, L0752: 1, L0731: 1 and L0757: 1.		
366	HLMDN29	881288	376	3 - 509	1276	Glu-15 to Glu-26, Thr-60 to Ile-66,	AR061: 5, AR089: 2 H0254: 1, H0255: 1,		

367	HWBCF78	911355	377	1 - 330	1277	Gly-82 to Tyr-88. Pro-1 to Gly-9, Pro-11 to Gly-18, Asp-35 to Arg-55.	H0705: 1 and H0412: 1. AR089: 1, AR061: 1 H0457: 12, H0521: 11, H0179: 6, H0402: 5, H0271: 3, H0581: 2, H0188: 2, S0002: 2, S0053: 2, H0522: 2, H0436: 2, H0254: 1, H0255: 1, H0306: 1, H0638: 1, H0637: 1, H0580: 1, H0619: 1, S0278: 1, H0587: 1, H0486: 1, S0049: 1, H0050: 1, H0510: 1, H0252: 1, H0553: 1, H0606: 1, S0142: 1, S0344: 1, H0529: 1, L0763: 1, L0770: 1, L0667: 1, L0767: 1, L0794: 1, L0774: 1, L0653: 1, L0659: 1, L0788: 1, S0052: 1, S0330: 1, H0555: 1, S0308: 1, L0592: 1, H0667: 1 and S0424: 1.		
368	HUKEN49	911465	378	92 - 340	1278	Pro-11 to Glu-17.	AR061: 1, AR089: 1 L0758: 19, L0777: 16, L0750: 14, L0747: 13, L0748: 10, H0692: 9, L0775: 6, L0749: 6,		

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									H0252: 1, H0615: 1, H0428: 1, T0006: 1, H0553: 1, L0055: 1, H0038: 1, H0551: 1, H0059: 1, H0100: 1, H0647: 1, S0142: 1, S0344: 1, H0529: 1, L0763: 1, L0770: 1, L0639: 1, L0761: 1, L0667: 1, L0641: 1, L0374: 1, L0767: 1, L0375: 1, L0383: 1, L0647: 1, L0792: 1, L0663: 1, L0664: 1, H0520: 1, H0547: 1, H0689: 1, H0682: 1, H0670: 1, S0378: 1, S0380: 1, H0555: 1, H0478: 1, S012: 1, L0742: 1, L0439: 1, L0754: 1, L0731: 1, L0592: 1, L0608: 1, H0543: 1, H0422: 1 and H0352: 1.				
369	HCUDS02	914401	379	63 - 860	1279	Pro-16 to Arg-23, Thr-148 to Leu-155, Phe-203 to Asp-214, Pro-255 to Ser-265.	AR089: 13, AR061: 6 S0354: 2, S0212: 1, H0484: 1, H0402: 1, S0358: 1, H0059: 1, H0494: 1, S0002: 1, L0438: 1, H0521: 1 and						

370	HTTJU40	914402	380	16 - 495	1280	Thr-71 to Leu-78, Phe-126 to Gly-133, Arg-150 to Gly-159.	L0751: 1. AR089: 1, AR061: 1 H0457: 1, H0213: 1, H0634: 1 and S0002: 1.		
371	HFXJX41	915649	381	296 - 682	1281	Arg-1 to Lys-10, Gln-39 to Asp-44.	AR061: 0, AR089: 0 S0282: 1, S0150: 1 and S0260: 1.		
372	HSLCK91	915650	382	1 - 399	1282		AR089: 1, AR061: 0 S0028: 2, S0142: 1 and S0344: 1.		
373	HSLAO29	917349	383	3 - 452	1283	Ala-40 to Leu-47, Gln-79 to Cys-84, Cys-95 to Thr-100.	AR061: 17, AR089: 4 H0556: 18, H0265: 8, H0692: 8, L0748: 7, H0543: 7, S0418: 6, L0665: 5, L0747: 5, H0445: 5, H0542: 5, H0318: 4, H0617: 4, L0769: 4, H0521: 4, L0750: 4, H0423: 4, H0135: 3, H0551: 3, H0560: 3, L0768: 3, L0766: 3, L0775: 3, L0776: 3, S0328: 3, S0314: 3, S0206: 3, L0439: 3, L0740: 3, L0591: 3, L0608: 3, H0170: 2, H0657: 2, H0484: 2, H0052: 2, H0545: 2, H0012: 2, H0620: 2, H0083: 2,	12q12-q14	123829, 147570, 181430, 252940, 264700, 600194, 600231, 600808, 601284, 601769, 601769, 602116

	H0040: 2, H0087: 2, S0144: 2, L0640: 2, L0771: 2, L0773: 2, L0521: 2, L0363: 2, L0783: 2, L0383: 2, L0663: 2, H0547: 2, L0751: 2, L0731: 2, L0757: 2, L0596: 2, L0595: 2, L0362: 2, H0422: 2, T0002: 1, H0686: 1, S0040: 1, S0218: 1, H0656: 1, H0341: 1, S0180: 1, S0212: 1, H0483: 1, H0177: 1, S0420: 1, S0356: 1, S0376: 1, S0360: 1, S0408: 1, H0208: 1, S0045: 1, S0046: 1, S0132: 1, L0717: 1, S0278: 1, H0331: 1, H0256: 1, T0109: 1, T0082: 1, H0309: 1, T0110: 1, H0327: 1, H0544: 1, H0041: 1, H0050: 1, S0051: 1, H0266: 1, H0252: 1, H0328: 1, H0604: 1, H0031: 1, H0644: 1, H0628: 1, H0181: 1, H0606: 1, S0364: 1, H0068: 1.	
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									H0124: 14, L0744: 4, S0036: 2, L0743: 2, L0759: 2, H0581: 1, H0457: 1, L0163: 1, H0616: 1, L0763: 1, L0776: 1, L0659: 1, L0783: 1, L0666: 1, L0750: 1 and L0779: 1.			
375	H0UES64	918119	385	3 - 317	1285	Pro-89 to Leu-102.			AR061: 1, AR089: 0 S0040: 1 and S0278: 1.			
376	HWLHU02	918520	386	3 - 398	1286	Gly-6 to Cys-12, Glu-48 to Asp-54, Ile-61 to Ser-73, Asn-75 to Thr-85, Gln-111 to Thr-118.			AR061: 2, AR089: 1 L0761: 2, L0791: 2, S0354: 1 and H0682: 1.			
377	HBAHA84	919363	387	84 - 794	1287	Pro-20 to Ala-30.			AR089: 46, AR061: 9			
378	HBMXQ90	922114	388	149 - 439	1288				AR089: 7, AR061: 6 S0116: 1, H0646: 1 and L0731: 1.			
379	HOEJV72	930778	389	77 - 817	1289	Leu-51 to Asp-57, Leu-91 to Lys-97, Asp-143 to Pro-148.			AR089: 6, AR061: 5 S0360: 9, L0642: 5, L0752: 5, L0662: 4, L0659: 4, L0666: 4, S0007: 3, L0646: 3, L0776: 3, L0750: 3, H0662: 2, S0222: 2, L0483: 2, L0764: 2, L0648: 2, L0775: 2, L0665: 2, H0648: 2,	1q22-q25	104770, 107300, 107670, 110700, 131210, 136132, 145001, 146790, 150292, 159440,	

380	HRDBH58	933364	390	455 - 2239	1290	L0779: 2, S0031: 2, S0110: 1, H0638: 1, S0418: 1, S0376: 1, S0444: 1, L0717: 1, H0331: 1, H0574: 1, S0414: 1, H0492: 1, H0156: 1, L0021: 1, S0049: 1, H0310: 1, H0327: 1, H0373: 1, T0010: 1, S6028: 1, H0615: 1, S0366: 1, S0036: 1, H0038: 1, H0616: 1, H0413: 1, T0041: 1, H0494: 1, S0438: 1, H0509: 1, S0142: 1, S0210: 1, L0598: 1, L0762: 1, L0640: 1, L0631: 1, L0772: 1, L0766: 1, L0551: 1, L0774: 1, L0664: 1, H0547: 1, S0126: 1, H0659: 1, S0378: 1, S0152: 1, S3014: 1, L0439: 1, L0740: 1, L0754: 1, L0756: 1, L0780: 1, L0755: 1, L0758: 1, S0434: 1, S0026: 1 and H0667: 1.	159440, 159440, 173610, 186780, 191030, 191315, 208250, 233710, 600923, 600995, 601412, 601518, 601652, 602491
						AR089: 1, AR061: 0	

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						Arg-96 to Asn-104.	H0670: 3, H0261: 2, S0222: 2, L0771: 2, L0803: 2, S0358: 1, S0360: 1, H0632: 1, H0575: 1, H0615: 1, H0059: 1, H0509: 1, L0772: 1, L0646: 1, L0764: 1, L0662: 1, L0805: 1, L0776: 1 and L0596: 1.			
383	HFXJW08	959204	393	170 - 580	1293	Val-12 to Arg-18, Thr-84 to Leu-90, Asp-103 to Gln-114.	AR089: 1, AR061: 0 S0282: 2 and H0135: 1.			
384	HBTAD04	407351	394	1 - 318	1294	Ser-10 to Gln-18.	AR089: 1, AR061: 0 S0180: 1, H0416: 1 and S0028: 1.			
385	HE8FG51	465267	395	1 - 267	1295	Arg-11 to Glu-20. Gly-1 to Ile-8, Pro-10 to Asp-16, Asn-19 to Tyr-25, Gly-42 to Lys-49, Ile-59 to Gly-66.	AR061: 4, AR089: 1 H0266: 2, H0013: 1 and L0758: 1.			
386	HTPDU31	503077	396	305 - 3	1296	Asp-3 to Gly-11.	AR061: 11, AR089: 8 S0007: 1, S0046: 1, H0052: 1, H0039: 1 and L0439: 1.			
387	HMUBV12	549423	397	64 - 306	1297		AR061: 2, AR089: 2 L0592: 2, H0013: 1, H0178: 1, H0099: 1, H0032: 1, H0529: 1,	3p21.3	116806, 120120, 120120, 120120,	

									L0772: 1, H0521: 1 and L0780: 1.		120436, 120436, 120436, 138320, 168468, 182280, 600163
388	HMHBS90	574062	398	40 - 618	1298	Arg-3 to Gln-14, Gln-25 to Gln-30.			AR061: 3, AR089: 3 L0747: 9, L0794: 5, L0789: 4, L0662: 3, L0803: 3, S0152: 3, L0439: 3, L0777: 3, L0757: 3, L0593: 3, H0624: 2, H0318: 2, H0673: 2, H0412: 2, L0800: 2, L0764: 2, L0776: 2, L0748: 2, H0171: 1, T0049: 1, H0657: 1, H0661: 1, H0449: 1, H0580: 1, H0619: 1, H0370: 1, H0156: 1, H0253: 1, H0052: 1, H0620: 1, H0201: 1, S0051: 1, T0010: 1, H0286: 1, H0688: 1, H0622: 1, H0181: 1, L0456: 1, H0135: 1, H0087: 1, H0264: 1, L0065: 1, H0633: 1, S0144: 1,		

389	HLHGH34	575733	399	2 - 436	1299	Phe-10 to Asn-18, Leu-80 to Ile-86, Ile-118 to Arg-123.	S0142: 1, H0529: 1, L0763: 1, L0770: 1, L0769: 1, L0761: 1, L0643: 1, L0644: 1, L0773: 1, L0767: 1, L0766: 1, L0381: 1, L0527: 1, L0659: 1, L0809: 1, L0666: 1, H0519: 1, H0593: 1, H0689: 1, H0435: 1, H0670: 1, S0037: 1, S0027: 1, L0779: 1, L0752: 1, L0758: 1, L0759: 1, L0595: 1, S0106: 1 and H0422: 1. AR061: 5, AR089: 2 S0007: 2, H0024: 2, L0749: 2, S0003: 1, H0659: 1, L0748: 1, L0740: 1, L0758: 1 and L0595: 1.	10p15.1		
390	HELHC55	577384	400	214 - 2	1300		AR061: 6, AR089: 2 S0001: 1 and S0045: 1.			
391	HKAAZ66	592105	401	3 - 434	1301	Arg-1 to Phe-19, Gln-22 to Arg-28, Leu-92 to Thr-108.	AR089: 2, AR061: 1 L0659: 13, L0731: 12, L0803: 9, L0439: 9, L0601: 8, S0152: 7, L0756: 7, H0551: 6, L0666: 5, L0747: 5, L0646: 4, L0375: 4,	1		

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H0002: 1, H0042: 1, H0575: 1, T0082: 1, S0474: 1, H0581: 1, H0421: 1, L0040: 1, H0327: 1, L0041: 1, H0123: 1, L0471: 1, H0373: 1, H0051: 1, H0275: 1, H0375: 1, S0003: 1, S0214: 1, H0615: 1, H0039: 1, L0483: 1, H0553: 1, S0364: 1, H0316: 1, H0598: 1, H0591: 1, H0477: 1, H0268: 1, S0386: 1, H0561: 1, H0646: 1, S0210: 1, H0695: 1, L0520: 1, L0640: 1, L0638: 1, L0796: 1, L0772: 1, L0373: 1, L0764: 1, L0648: 1, L0364: 1, L0794: 1, L0774: 1, L0651: 1, L0523: 1, L0805: 1, L0653: 1, L0657: 1, L0538: 1, L0519: 1, L0544: 1, L0789: 1, L0663: 1, L0664: 1, S0052: 1, S0428: 1, H0144: 1, H0684: 1, H0435: 1, H0658: 1, H0648: 1.

								S0378: 1, H0696: 1, H0704: 1, H0436: 1, S0390: 1, S3014: 1, S0028: 1, L0777: 1, L0755: 1, H0445: 1, L0588: 1, L0605: 1, L0485: 1, S0026: 1, S0192: 1, S0194: 1, H0542: 1, S0412: 1 and H0352: 1.			
392	HHSCN33	657367	402	1 - 396	1302			AR089: 2, AR061: 1 H0013: 1, S0010: 1, S0051: 1 and L0741: 1.			
393	HNGJQ15	660310	403	1 - 207	1303	His-51 to Gly-56.		AR061: 8, AR089: 5 S0052: 1 and H0136: 1.	2q37.2		
394	HDJME16	661396	404	1 - 486	1304	Ser-8 to Ala-16, Leu-51 to Gln-56, Tyr-61 to Ala-73, Ala-77 to Thr-83, Gln-90 to Glu-104, Glu-118 to Asp-127.		AR061: 1, AR089: 0 S0360: 2, H0553: 2, L0776: 2, L0744: 2, L0747: 2, L0750: 2, H0542: 2, S0110: 1, S0400: 1, H0441: 1, H0392: 1, H0156: 1, S0051: 1, H0687: 1, H0135: 1, H0087: 1, H0647: 1, L0631: 1, L0638: 1, L0774: 1, L0775: 1, L0659: 1, H0547: 1, S0380: 1, S0332: 1, L0743: 1, L0749: 1 and L0777: 1.	3q21-q25	106165, 117700, 117700, 150210, 169600, 180380, 180380, 180380, 190000, 203500, 222900, 232050, 276902, 600882, 601199,	

395	HNTNR64	670033	405	3 - 365	1305	Asp-19 to Trp-25.	AR089: 1, AR061: 0 L0749: 8, L0759: 6, L0789: 3, L0748: 3, H0624: 2, L0471: 2, H0266: 2, H0170: 1, H0171: 1, S0360: 1, S0222: 1, H0441: 1, H0333: 1, H0013: 1, H0244: 1, H0251: 1, H0014: 1, H0553: 1, H0032: 1, S0036: 1, S0306: 1, S0150: 1, L0766: 1, L0653: 1, H0144: 1, H0520: 1, H0593: 1, H0690: 1, H0660: 1, S0380: 1, H0518: 1, H0521: 1, S0032: 1, L0439: 1, L0740: 1, L0751: 1, L0750: 1, L0756: 1, L0731: 1, L0589: 1, H0668: 1 and H0293: 1.			601199, 601199, 601471, 601682
396	HMICO24	677036	406	1 - 303	1306	Arg-7 to Trp-13, Thr-18 to Trp-29, Gly-55 to Ser-60.	AR061: 9, AR089: 7 L0766: 9, L0731: 5, S6028: 2, L0779: 2, H0650: 1 S0001: 1			

								S0222: 1, L0021: 1, H0553: 1, H0551: 1, H0488: 1, S0426: 1, L0803: 1, L0784: 1, L0783: 1, L0666: 1, S0374: 1, H0365: 1, H0659: 1, H0539: 1, H0555: 1, L0777: 1, L0758: 1, L0366: 1 and H0506: 1.			
397	HSIAC23	679292	407	92 - 424	1307	Arg-34 to Thr-40, Asp-79 to Gly-90.		AR061: 0, AR089: 0 L0439: 8, L0438: 7, L0666: 4, H0685: 1, S0376: 1, S0360: 1, L0444: 1, L0021: 1, H0036: 1, H0553: 1, L0772: 1, L0771: 1, L0768: 1, L0774: 1, L0651: 1, L0659: 1, H0684: 1, H0672: 1 and L0754: 1.	9q21.11-21.33	602014	
398	HSLFL74	685897	408	3 - 473	1308			AR089: 1, AR061: 0 S0028: 2, S0218: 1, S0001: 1 and S0390: 1.			
399	HSDJD53	698259	409	163 - 624	1309	Ala-29 to Leu-35, Ala-45 to Pro-53, Ser-80 to Arg-89, Val-111 to Cys-118.		AR089: 2, AR061: 0 H0687: 2, S0050: 1, S0028: 1, S0031: 1 and S0260: 1.			
400	HCEBF33	702955	410	3 - 581	1310			AR061: 6, AR089: 4 L0439: 2, H0052: 1,			

401	HAPQW27	705518	411	1 - 327	1311	Asn-3 to Arg-11, Gln-42 to Asp-50.	H0644: 1, H0520: 1 and L0756: 1. AR061: 4, AR089: 1 L0748: 5, L0744: 4, L0751: 4, H0039: 3, H0617: 3, L0646: 3, L0809: 3, L0779: 3, H0295: 2, H0255: 2, S0358: 2, H0575: 2, H0457: 2, H0181: 2, H0673: 2, L0637: 2, L0743: 2, L0750: 2, L0758: 2, S0116: 1, H0663: 1, S0356: 1, S0376: 1, S0360: 1, H0675: 1, S0007: 1, H0497: 1, H0590: 1, H0618: 1, H0253: 1, H0545: 1, S0051: 1, H0622: 1, H0030: 1, H0135: 1, H0538: 1, S0426: 1, H0529: 1, L0763: 1, L0769: 1, L0764: 1, L0771: 1, L0773: 1, L0775: 1, L0788: 1, L0663: 1, H0144: 1, L0438: 1, H0690: 1, H0670: 1, H0672: 1, S0328: 1, S0406: 1, H0187: 1,	8qter	
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402	HCFLZ28	707183	412	133 - 513	1312	Glu-46 to Gly-54, Val-64 to Ala-69, Glu-74 to Leu-79, Glu-90 to Glu-97.	L0747: 1, L0749: 1, L0759: 1 and L0608: 1. AR089: 2, AR061: 1 H0556: 8, L0596: 8, L0588: 6, H0618: 5, H0266: 5, H0038: 5, H0616: 5, H0547: 5, L0740: 5, H0265: 4, S0022: 4, H0591: 4, H0529: 4, L0769: 4, L0766: 4, L0664: 4, H0521: 4, L0747: 4, S0420: 3, H0497: 3, H0253: 3, H0031: 3, H0135: 3, H0264: 3, H0056: 3, H0494: 3, L0657: 3, L0438: 3, L0748: 3, L0777: 3, L0758: 3, H0543: 3, H0624: 2, H0656: 2, S0418: 2, S0007: 2, H0333: 2, H0013: 2, S0010: 2, H0596: 2, L0471: 2, H0083: 2, H0039: 2, H0622: 2, H0617: 2, H0068: 2, H0163: 2, H0623: 2, H0100: 2, L0369: 2, L0763: 2, L0764: 2, L0378: 2, L0656: 2,				
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												L0770: 1, L0646: 1, L0773: 1, L0662: 1, L0768: 1, L0381: 1, L0803: 1, L0804: 1, L0651: 1, L0653: 1, L0606: 1, L0527: 1, L0659: 1, L0526: 1, L0519: 1, S0006: 1, S0374: 1, H0519: 1, S0126: 1, H0711: 1, S0328: 1, S0152: 1, H0696: 1, H0626: 1, H0627: 1, L0752: 1, L0755: 1, L0757: 1, H0445: 1, L0591: 1, L0581: 1, L0601: 1, H0665: 1, H0136: 1, S0192: 1, H0423: 1, L0697: 1, S0424: 1 and H0293: 1.					
403	HWCAB58	710377	413	3 - 449	1313	Lys-14 to Leu-21.	AR089: 13, AR061: 6 L0759: 2, H0012: 1, S0294: 1, L0809: 1, L0791: 1 and L0777: 1.										
404	HLMCMC57	713770	414	221 - 478	1314		H0255: 2, H0163: 1, H0691: 1 and L0747: 1.										
405	HMEHLH37	717556	415	163 - 558	1315	Asp-34 to Ser-44.	AR089: 2, AR061: 1										
406	HNGJI55	722240	416	1 - 303	1316	Arg-1 to Asp-11, Thr-15 to Thr-21.	AR050: 48, AR054: 42, AR051: 37, AR061:										

						Pro-93 to Glu-101.	6, AR089: 3 H0164: 1, S0052: 1 and S0031: 1.		
	868063	869	218 - 646	1769		His-8 to Gly-18, Glu-30 to Asp-36, Thr-40 to Thr-46, Pro-118 to Ala-133.			
407	HHGDG42	724795	417	128 - 358	1317		AR061: 47, AR089: 2		
408	HMTMF31	731302	418	50 - 424	1318		AR089: 1, AR061: 0 H0525: 1		
409	HSDIF59	739212	419	282 - 752	1319	Pro-19 to Thr-31, Asp-137 to Ser-143.	AR089: 4, AR061: 2 S0218: 1, S0222: 1, H0617: 1, S0150: 1 and S0260: 1.		
410	HNDAG60	751953	420	174 - 365	1320	Ser-9 to Asp-15, Glu-20 to Asp-28, Glu-34 to Cys-40.	AR089: 14, AR061: 7 H0031: 2, H0624: 1, S0116: 1, S0354: 1, S0045: 1, H0581: 1, H0046: 1, H0428: 1, H0038: 1, H0494: 1, H0517: 1 and S0053: 1.		
411	HSLDS79	753247	421	99 - 1646	1321	Pro-5 to Lys-12, Ala-31 to Pro-41, Phe-58 to Thr-63, Gln-83 to Phe-89, Pro-102 to Leu-116, Ser-130 to Asp-138, Pro-196 to Gln-208, Tyr-231 to Ala-240,	AR050: 10, AR051: 4, AR054: 3, AR089: 1, AR061: 1 H0544: 1 and S0028: 1.		

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										T0082: 1, H0009: 1, H0083: 1, H0510: 1, H0266: 1, H0135: 1, T0041: 1, H0494: 1, L0369: 1, L0667: 1, L0800: 1, L0774: 1, L0787: 1, H0547: 1, L0747: 1, L0759: 1, L0593: 1 and S0424: 1.			
415	HPHAF45	812327	425	1 - 384	1325	Cys-26 to Trp-34, Phe-111 to Asp-119.				AR089: 1, AR061: 0 H0619: 1, H0431: 1, S0148: 1, H0519: 1, L0589: 1, L0591: 1 and L0594: 1.			
416	HSUME31	812373	426	1 - 441	1326	Thr-2 to Arg-7, Asp-37 to Trp-42.				AR061: 168, AR089: 115 H0556: 6, H0265: 4, H0040: 4, S0418: 2, S0420: 2, H0266: 2, H0038: 2, T0002: 1, T0049: 1, S0045: 1, S0046: 1, S0022: 1, H0256: 1, H0486: 1, H0634: 1, L0766: 1, S0052: 1, S0126: 1, H0539: 1, S0037: 1, S0027: 1, L0743: 1, L0751: 1, L0749: 1, L0731: 1, L0591: 1, L0595: 1, H0136: 1,			

417	HUSHB56	815819	427	2 - 412	1327	Pro-8 to Arg-14, Glu-16 to Arg-23, Gly-25 to Pro-30, Arg-59 to Glu-69, Pro-78 to Glu-83.	S0276: 1 and H0543: 1. AR089: 2, AR061: 1 H0437: 1 and H0538: 1.		
418	HTGDN81	824708	428	390 - 1031	1328		AR050: 9, AR054: 3, AR051: 1, AR061: 0, AR089: 0 S0028: 2, S0134: 1, S0132: 1 and S0222: 1.		
419	HSKHY26	836598	429	2 - 571	1329		AR089: 1, AR061: 0 H0478: 3, S0278: 2, L0731: 2, S0001: 1, S0360: 1, S0132: 1, H0619: 1, H0263: 1, S0036: 1, H0040: 1, H0494: 1, S0142: 1, S0344: 1, L0764: 1, L0766: 1, S3014: 1, L0748: 1, H0445: 1 and S0434: 1.	12q13	107777, 123940, 139350, 139350, 148040, 148041, 148043, 148070, 231550, 600194, 600231, 600536, 600808, 600956, 601284, 601769, 601769, 601928, 602116,

420	HKACD80	837698	430	72 - 536	1330	Pro-34 to Val-40, Thr-65 to Asp-70.	AR089: 12, AR061: 6 L0766: 4, H0052: 3, L0662: 3, L0776: 3, L0666: 3, L0665: 3, H0521: 3, H0438: 2, H0581: 2, H0263: 2, H0494: 2, L0763: 2, L0770: 2, L0769: 2, L0649: 2, L0664: 2, L0748: 2, L0439: 2, L0747: 2, S0436: 2, H0265: 1, H0556: 1, S0040: 1, H0656: 1, S0444: 1, S0278: 1, H0415: 1, H0403: 1, H0643: 1, S0280: 1, H0575: 1, H0194: 1, H0309: 1, H0545: 1, H0046: 1, L0157: 1, H0375: 1, L0483: 1, H0553: 1, H0412: 1, H0646: 1, S0002: 1, L0796: 1, L0644: 1, L0764: 1, L0774: 1, L0376: 1, L0806: 1, L0654: 1, L0659: 1, L0383: 1, H0547: 1, S0126: 1, H0684: 1, H0435: 1, H0478: 1,		602153
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								S0028: 1, L0751: 1, L0754: 1, L0749: 1, L0750: 1, L0779: 1, L0759: 1, H0543: 1 and H0423: 1.			
421	HHFDK48	837782	431	1 - 384	1331	Asn-1 to Gly-8, His-10 to Lys-15, Gly-96 to Cys-102, Pro-104 to Phe-109.		AR089: 257, AR061: 210 H0050: 1, L0194: 1 and H0555: 1.			
422	HE9SS77	838043	432	3 - 725	1332	Leu-1 to Tyr-8, Lys-21 to Asn-27, Asn-33 to Thr-49.		AR089: 102, AR061: 58 H0013: 1, S0250: 1, S0022: 1, H0038: 1, L0659: 1, H0144: 1 and S0390: 1.			
423	HAPOK49	848205	433	123 - 1031	1333			AR061: 8, AR089: 6 H0641: 9, L0748: 6, L0731: 5, L0777: 4, L0758: 4, L0771: 3, L0755: 3, H0638: 2, H0622: 2, L0769: 2, L0637: 2, L0662: 2, L0766: 2, L0775: 2, S0126: 2, H0518: 2, H0521: 2, H0522: 2, S0206: 2, L0779: 2, H0423: 2, T0002: 1, H0657: 1, L0785: 1, H0661: 1, L0562: 1, L0539: 1, S0356: 1,			

									L0622: 1, H0486: 1, H0427: 1, H0575: 1, H0004: 1, H0083: 1, H0109: 1, H0039: 1, H0617: 1, H0090: 1, H0063: 1, H0130: 1, S0002: 1, S0426: 1, L0763: 1, L0770: 1, L0761: 1, L0772: 1, L0372: 1, L0764: 1, L0768: 1, L0774: 1, L0776: 1, L0655: 1, L0659: 1, L0542: 1, L0789: 1, L0666: 1, L0663: 1, L0438: 1, H0435: 1, S0044: 1, S0404: 1, H0187: 1, H0478: 1, L0747: 1, L0759: 1, L0591: 1 and H0543: 1.				
424	HPMGN48	848318	434	3 - 635	1334	His-1 to Thr-6, Pro-14 to Trp-21, Glu-43 to Gly-50, Asp-97 to Gly-103, Glu-141 to Asp-149, Ile-199 to Gly-204.		AR089: 15, AR061: 5, H0550: 2, L0662: 2, H0657: 1, H0662: 1, H0619: 1, S0474: 1, H0081: 1, L0471: 1, H0428: 1, H0031: 1, H0063: 1, H0494: 1, L0642: 1, L0666: 1, L0748: 1 and L0747: 1.					
425	HUVHP54	849278	435	258 - 1001	1335	Glu-86 to Asp-93.		AR061: 7, AR089: 7					

426	HSLDK59	853385	436	491 - 1009	1336	Glu-18 to Lys-24, Pro-68 to Gly-75, Tyr-122 to Arg-136, Pro-148 to Glu-158.	Trp-100 to Asp-110, Asp-163 to Asn-172.	S0358: 5, H0590: 2, H0623: 2, L0803: 2, S0152: 2, S3014: 2, L0754: 2, H0458: 1, S0354: 1, H0549: 1, H0431: 1, H0497: 1, H0042: 1, H0036: 1, H0581: 1, H0196: 1, T0115: 1, H0024: 1, H0275: 1, H0622: 1, S0364: 1, H0124: 1, H0056: 1, H0429: 1, S0150: 1, L0640: 1, L0642: 1, L0804: 1, L0666: 1, S0330: 1, H0478: 1, S0027: 1, S0206: 1, L0592: 1, L0604: 1 and S0424: 1.		
427	HMWDI41	854051	437	2 - 613	1337	Ile-30 to Cys-36, Pro-56 to Gly-65, Glu-105 to Glu-110.		AR061: 1, AR089: 1 S0028: 3, S0222: 2, L0105: 2, S0050: 2, S0390: 2, S0260: 2, H0344: 1, H0381: 1, S0282: 1, H0618: 1, S0051: 1, S6028: 1, H0271: 1, H0383: 1, H0264: 1 and S0038: 1.		

428	HFVHU73	856165	438	3 - 314	1338	Val-34 to Lys-56, Pro-65 to Asp-73, Thr-79 to Asn-84.	Tyr-170 to Arg-175, Asp-183 to Trp-189.	H0341: 1, S0358: 1, H0051: 1, S0210: 1, H0529: 1, L0803: 1, H0539: 1, H0521: 1, H0436: 1, L0779: 1, L0366: 1 and H0506: 1. AR089: 6, AR061: 1 H0341: 1, H0393: 1 and H0266: 1.		
429	HMUBJ80	858497	439	517 - 2	1339			AR089: 16, AR061: 4 L0748: 9, L0439: 5, L0717: 4, L0659: 4, L0663: 4, H0658: 4, S0045: 3, L0766: 3, L0744: 3, L0749: 3, L0758: 3, H0542: 3, H0265: 2, H0556: 2, S0040: 2, H0458: 2, H0587: 2, H0486: 2, H0318: 2, H0052: 2, H0687: 2, L0770: 2, L0769: 2, L0646: 2, L0666: 2, H0682: 2, L0756: 2, L0752: 2, L0731: 2, L0608: 2, H0543: 2, H0423: 2, H0656: 1, H0402: 1, S0418: 1, S0420: 1, S0360: 1, H0619: 1, H0392: 1, H0643: 1.		

430	HE9ML74	859297	440	3 - 959	1340	Asp-8 to Asp-20, Phe-43 to Arg-52, Ser-102 to Asp-107, His-109 to Asn-124	AR061: 1, AR089: 1 L0803: 9, L0758: 7, L0439: 6, L0740: 5, L0766: 4 L0666: 4	AR061: 1, AR089: 1 L0803: 9, L0758: 7, L0439: 6, L0740: 5, L0766: 4 L0666: 4	
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Phe-131 to Lys-136, Pro-143 to Pro-149, Lys-189 to Leu-200, Asn-305 to Trp-310.	L0663: 4, L0754: 4, L0747: 4, L0804: 3, H0144: 3, L0750: 3, L0756: 3, L0752: 3, L0600: 3, S0003: 2, L0455: 2, S0366: 2, H0529: 2, L0659: 2, L0809: 2, L0665: 2, H0547: 2, H0672: 2, H0539: 2, L0748: 2, L0759: 2, L0591: 2, L0485: 2, S0040: 1, H0650: 1, H0656: 1, S0212: 1, H0663: 1, S0360: 1, H0351: 1, S0222: 1, S6014: 1, H0392: 1, H0632: 1, T0114: 1, H0427: 1, L0021: 1, H0599: 1, H0575: 1, H0581: 1, S0049: 1, L0471: 1, H0373: 1, H0510: 1, S6028: 1, H0615: 1, H0622: 1, S0036: 1, T0067: 1, H0413: 1, T0041: 1, S0002: 1, S0426: 1, L0369: 1, L0770: 1, L0769: 1, L0761: 1, L0772: 1, L0646: 1, L0794: 1, L0774: 1, L0775: 1.
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								L0655: 1, L0661: 1, L0647: 1, L0792: 1, L0793: 1, L0664: 1, H0682: 1, H0435: 1, H0659: 1, H0660: 1, H0651: 1, S0013: 1, H0436: 1, L0779: 1, L0608: 1, S0446: 1 and H0506: 1.			
431	HLQAJ01	864092	441	1 - 300	1341	Pro-56 to Arg-67, Asp-86 to Gly-98.		AR089: 14, AR061: 10 L0803: 4, L0764: 2, L0794: 2, H0331: 1, H0574: 1, H0486: 1, H0318: 1, H0264: 1, L0804: 1, L0809: 1, L0665: 1, L0438: 1, H0684: 1, L0759: 1 and L0584: 1.			
432	HSLDP32	866241	442	12 - 257	1342	Asn-6 to Lys-13.		AR089: 1, AR061: 0 S0028: 2, H0135: 1, H0163: 1 and S0044: 1.			
433	HPMEG40	866272	443	270 - 611	1343	Val-1 to Leu-7, Arg-49 to Trp-59.		AR089: 0, AR061: 0 S0028: 4, S0390: 2, S0300: 1, H0031: 1, S0144: 1 and S0032: 1.			
434	HRADE27	867195	444	2 - 547	1344	Glu-33 to Pro-38.		AR089: 1, AR061: 0 L0435: 2, H0624: 1, L0717: 1, S0214: 1, L0662: 1, L0766: 1, L0803: 1, S0380: 1,			

435	HTXQR10	869137	445	76 - 537	1345	Ser-38 to Thr-46.	AR061: 5, AR089: 3 H0250: 4, L0745: 4, L0746: 4, L0766: 3, L0666: 2, L0758: 2, H0556: 1, S0418: 1, H0486: 1, H0052: 1, H0252: 1, H0181: 1, H0116: 1, H0412: 1, S0210: 1, L0764: 1, L0794: 1 and H0672: 1.	H0555: 1, L0754: 1 and L0756: 1.	
436	HEQCB27	871062	446	1 - 423	1346		AR089: 19, AR061: 3 H0544: 1 and S0036: 1.		
437	HE8AM04	871156	447	3 - 518	1347		AR061: 223, AR089: 167 H0013: 2, H0135: 1 and H0633: 1.		
438	HSLHT48	871996	448	81 - 542	1348	Pro-17 to Ala-22.	AR061: 1, AR089: 1 S0028: 2, S0045: 1, S6026: 1, H0231: 1, S0050: 1, H0617: 1, H0189: 1 and S0144: 1.		
439	HS2SH70	875870	449	193 - 1014	1349	Thr-5 to Gln-52, Lys-121 to Ile-134.	AR089: 1, AR061: 1 H0124: 5, T0040: 2, H0144: 2, S0342: 1, S0046: 1, H0550: 1, H0455: 1, H0486: 1, H0575: 1, T0110: 1, H0046: 1, H0266: 1.		

									H0316: 1, H0616: 1, H0551: 1, T0041: 1, H0561: 1, L0438: 1, H0547: 1, S0152: 1, H0521: 1, H0555: 1, H0631: 1 and L0731: 1.			
440	HAOAE45	876157	450	3 - 440	1350				AR089: 414, AR061: 79 L0751: 2, H0341: 1, S0132: 1, H0550: 1, S0222: 1, H0431: 1, H0046: 1, L0471: 1, H0083: 1, S0314: 1, H0031: 1, H0644: 1, H0488: 1, H0413: 1, T0041: 1, S0150: 1, S0344: 1, L0662: 1, L0657: 1, L0663: 1, S0374: 1, H0519: 1, L0748: 1 and L0592: 1.			
441	HELBA42	878549	451	69 - 695	1351	Lys-35 to Gln-40, Gln-61 to Lys-66, Ser-116 to Gly-121, Gln-192 to Ser-205.			AR089: 53, AR050: 32, AR054: 28, AR051: 24, AR061: 19 L0439: 3, S0212: 2, H0052: 2, S0051: 2, L0805: 2, H0435: 2, H0624: 1, H0265: 1, H0686: 1, S0420: 1, S0045: 1, S0300: 1, S0222: 1, H0069: 1,			

								H0581: 1, L0157: 1, T0010: 1, H0355: 1, H0266: 1, H0428: 1, T0041: 1, L0475: 1, H0130: 1, S0210: 1, S0002: 1, L0788: 1 and L0759: 1.			
442	HSPBB15	878791	452	1 - 564	1352	Gly-19 to Thr-24.		AR089: 10, AR061: 2 H0484: 2, H0052: 1 and H0478: 1.			
443	HTAFF91	879399	453	3 - 431	1353	Gly-1 to Cys-6.		AR089: 4, AR061: 0 H0305: 2, H0587: 1 and H0069: 1.			
444	HETHB58	879640	454	28 - 669	1354	Ser-28 to Val-35, Arg-49 to Arg-57.		AR061: 4, AR089: 2 H0539: 5, L0758: 4, H0620: 3, L0809: 3, H0050: 2, S0002: 2, L0803: 2, L0805: 2, S0330: 2, L0754: 2, L0755: 2, L0605: 2, H0265: 1, H0556: 1, S0040: 1, H0341: 1, S0212: 1, S0110: 1, S0360: 1, H0645: 1, S0278: 1, H0431: 1, H0497: 1, H0013: 1, H0618: 1, H0581: 1, H0052: 1, H0544: 1, H0046: 1, H0024: 1, H0051: 1, S0250: 1,			

445	HGBCU40	880328	455	93 - 533	1355	Pro-1 to Lys-12, Gln-29 to Arg-34, Asn-37 to Tyr-48, Asn-54 to Ser-63, Pro-68 to Leu-73, Asp-125 to Gln-135.	S0022: 1, H0622: 1, L0142: 1, H0124: 1, S0344: 1, L0770: 1, L0761: 1, L0794: 1, L0774: 1, L0776: 1, L0656: 1, L0659: 1, L0789: 1, L0666: 1, L0665: 1, S0428: 1, H0519: 1, S0126: 1, H0435: 1, H0555: 1, S3014: 1, S0028: 1, L0756: 1, L0777: 1, S0031: 1, H0445: 1 and L0596: 1.		
446	HE9PR39	882939	456	3 - 500	1356	Pro-8 to Gly-17, Arg-22 to Ser-29.	AR089: 2, AR061: 1 H0251: 4, H0024: 2, H0341: 1, S0418: 1, H0015: 1, S0013: 1 and L0601: 1.		
447	HTEAF36	839516	457	68 - 316	1357		AR061: 4, AR089: 2 H0013: 4, L0740: 3, H0163: 2, L0768: 2, L0593: 2, H0624: 1, H0171: 1, S0003: 1, T0006: 1, L0776: 1, H0144: 1, H0547: 1, L0750: 1, L0759: 1 and L0592: 1.		

H0529: 16, S0358: 14,
H0494: 14, L0755: 14,
L0665: 11, L0747: 11,
L0752: 11, H0521: 10,
S0360: 8, L0662: 8,
L0659: 8, H0435: 8,
L0439: 8, L0649: 7,
L0754: 7, L0601: 7,
H0663: 6, S0376: 6,
H0618: 6, L0637: 6,
L0646: 6, L0766: 6,
L0666: 6, H0295: 5,
H0661: 5, T0023: 5,
L0653: 5, S0380: 5,
L0758: 5, S0356: 4,
H0592: 4, H0586: 4,
H0497: 4, H0604: 4,
H0038: 4, L0772: 4,
L0768: 4, L0657: 4,
S0374: 4, H0685: 3,
S0442: 3, S0444: 3,
H0580: 3, H0253: 3,
H0581: 3, H0620: 3,
H0615: 3, H0031: 3,
H0617: 3, H0488: 3,
H0641: 3, H0647: 3,
L0794: 3, L0664: 3,
H0593: 3, L0748: 3,
L0750: 3, L0596: 3,
H0294: 2, H0656: 2,
H0483: 2, H0664: 2,

	H0673: 1, H0169: 1, H0674: 1, S0036: 1, H0040: 1, H0616: 1, T0067: 1, H0560: 1, H0625: 1, S0466: 1, S0440: 1, S0150: 1, S0472: 1, S0144: 1, S0002: 1, L0640: 1, L0770: 1, L0761: 1, L0764: 1, L0363: 1, L0364: 1, L0774: 1, L0775: 1, L0375: 1, L0806: 1, L0805: 1, L0776: 1, L0655: 1, L0493: 1, L0636: 1, L0383: 1, L0809: 1, L0663: 1, S0052: 1, H0693: 1, H0547: 1, S0126: 1, H0690: 1, H0682: 1, H0683: 1, H0684: 1, H0659: 1, H0648: 1, H0672: 1, S0152: 1, S0350: 1, H0522: 1, S0392: 1, S0432: 1, L0741: 1, L0751: 1, L0745: 1, L0757: 1, S0434: 1, S0436: 1, L0592: 1, L0599: 1, L0361: 1, L0603: 1, S0460: 1, S0446: 1, H0506: 1 and	
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448	HTLGV66	839517	871	253 - 501	1771	Leu-21 to Phe-27, Gly-61 to Ala-68, Ala-85 to His-91, Asp-96 to Val-101, Asp-117 to Ile-131, Ala-155 to Ser-161.	L0600: 1.		
		883195	872	1 - 669	1772				
448	HTLGV66	883855	458	3 - 1085	1358	Glu-1 to Gln-19, Arg-58 to Pro-67, Glu-78 to Phe-85, Ser-104 to Arg-114, Arg-121 to Lys-130, Arg-135 to Thr-140, Asn-159 to Ser-168.	AR061: 1, AR089: 1 L0601: 2, H0618: 1, H0085: 1 and H0024: 1.	2q37.2	
449	HPJDV95	888844	459	362 - 1906	1359	Thr-12 to Ser-19, Val-22 to Glu-32, His-34 to Lys-43, Glu-129 to Lys-134, Phe-221 to Gln-226, Pro-231 to Pro-236, Lys-288 to Lys-299, Glu-320 to Gln-327, Thr-448 to Pro-455, Thr-490 to Glu-495.	AR061: 6, AR089: 2 H0457: 5, L0439: 4, H0013: 3, H0244: 3, H0266: 3, L0748: 3, H0556: 2, H0052: 2, H0040: 2, L0741: 2, L0740: 2, L0747: 2, L0759: 2, H0543: 2, H0265: 1, S0356: 1, H0580: 1, S0132: 1, H0619: 1, S0222: 1, T0082: 1, H0036: 1, H0421: 1, H0046: 1, H0009: 1, H0620: 1, T0010: 1, H0083: 1,		

									H0179: 1, H0271: 1, H0416: 1, S0250: 1, H0168: 1, H0634: 1, H0551: 1, S0386: 1, T0042: 1, H0641: 1, S0344: 1, L0766: 1, L0776: 1, L0565: 1, H0539: 1, S0152: 1, H0478: 1, L0754: 1, L0755: 1, H0707: 1, L0596: 1, L0605: 1, L0599: 1, H0542: 1, H0423: 1, H0422: 1 and H0506: 1.		
450	HCROF75	889436	460	48 - 533	1360	Ser-14 to Trp-22.	AR089: 29, AR061: 15 L0742: 2, S0356: 1, S0358: 1, S0360: 1, H0617: 1, H0040: 1 and H0522: 1.				
451	HDPAP15	909703	461	131 - 1120	1361	Arg-147 to Asn-153, Arg-165 to Glu-174, Phe-217 to Lys-222, Ala-306 to Ser-313.	AR089: 5, AR061: 2 L0755: 6, H0521: 5, H0634: 4, L0771: 4, L0766: 4, L0759: 4, L0800: 3, L0774: 3, H0659: 3, L0748: 3, L0754: 3, H0171: 2, H0550: 2, H0587: 2, H0264: 2, L0764: 2, L0768: 2, L0803: 2, L0775: 2, L0517: 2,				

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452	HTGDH34	896571	462	261 - 112	1362	Lys-6 to Gly-12.	L0746: 1, L0747: 1, L0750: 1, L0757: 1, L0758: 1, H0445: 1, S0026: 1 and S0276: 1. AR089: 10, AR061: 6 L0766: 10, L0758: 10, L0755: 8, L0731: 6, H0616: 5, L0740: 5, H0494: 4, H0696: 4, L0756: 4, L0752: 4, L0757: 4, S0358: 3, H0038: 3, L0770: 3, L0775: 3, S0328: 3, L0747: 3, H0662: 2, H0638: 2, H0580: 2, S0280: 2, H0052: 2, H0266: 2, T0067: 2, L0809: 2, L0666: 2, S0126: 2, H0435: 2, H0648: 2, H0521: 2, L0744: 2, L0748: 2, L0751: 2, L0749: 2, L0750: 2, L0684: 2, H0423: 2, S0040: 1, S0134: 1, H0657: 1, H0341: 1, S0212: 1, H0125: 1, H0370: 1, H0587: 1, H0486: 1, T0109: 1, H0250: 1, L0021: 1, H0098: 1.		
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454	HDPVG08	914973	464	3 - 1715	1364	Val-6 to Arg-16, Asp-25 to Thr-34.	L0764: 2, L0751: 2, H0295: 1, H0662: 1, H0240: 1, H0241: 1, H0675: 1, L0717: 1, S0222: 1, H0441: 1, H0036: 1, H0253: 1, T0023: 1, S0038: 1, L0662: 1, H0547: 1, H0555: 1, L0743: 1, L0749: 1 and L0758: 1.	1q32	114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580, 145260, 150310, 150310, 179820, 191045, 600105, 600759, 601494, 601975
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H0622: 2, H0031: 2, H0628: 2, H0591: 2, H0038: 2, T0041: 2, S0422: 2, L0640: 2, L0638: 2, L0772: 2, L0662: 2, L0804: 2, L0784: 2, L0659: 2, L0517: 2, L0519: 2, S0052: 2, S0126: 2, L0745: 2, L0750: 2, L0780: 2, L0605: 2, H0395: 1, S0114: 1, H0664: 1, H0638: 1, S0348: 1, S0418: 1, S0444: 1, H0645: 1, H0393: 1, H0613: 1, H0587: 1, H0643: 1, H0574: 1, H0250: 1, H0069: 1, S0346: 1, S0049: 1, H0052: 1, H0596: 1, H0123: 1, L0471: 1, S0388: 1, S0214: 1, H0428: 1, H0030: 1, H0617: 1, H0032: 1, H0673: 1, L0455: 1, H0598: 1, H0634: 1, H0616: 1, H0264: 1, H0413: 1, H0059: 1, H0131: 1, H0641: 1, S0210: 1, H0529: 1, L0763: 1.

									L0761: 1, L0764: 1, L0771: 1, L0521: 1, L0649: 1, L0650: 1, L0661: 1, L0384: 1, L0809: 1, L0647: 1, L0788: 1, L0789: 1, L0666: 1, L0663: 1, L0665: 1, S0428: 1, S0374: 1, H0519: 1, H0658: 1, H0648: 1, S0328: 1, S0330: 1, S0152: 1, H0696: 1, S0044: 1, H0436: 1, H0478: 1, H0540: 1, L0752: 1, L0753: 1, L0759: 1, S0031: 1, H0707: 1, L0608: 1, L0595: 1, S0026: 1, H0423: 1, L0697: 1, S0424: 1 and H0506: 1.				
455	HFXDW32	916095	465	2 - 886	1365	Gly-11 to Lys-20, His-41 to Cys-47, Thr-82 to Lys-90.			S0001: 2, H0624: 1, H0689: 1 and S0028: 1.				
456	HSSCY03	916445	466	2 - 1345	1366				L0741: 4, L0744: 4, H0556: 3, S0344: 3, L0763: 3, L0766: 3, L0743: 3, L0754: 3, L0747: 3, L0758: 3, L0596: 3, S0212: 2, H0662: 2, S0358: 2,				

457	HFXFI49	916758	467	139 - 615	1367	Lys-20 to Ile-29, Arg-46 to Pro-59, Ile-86 to Asn-93, Phe-115 to Asn-120.	AR061: 2, AR089: 1 S0028: 4, S0001: 2, S0282: 2, S0278: 2, S0050: 2, H0416: 1, H0027: 1, S0038: 1, S0052: 1, S0053: 1, H0684: 1 and S0044: 1.		
							S0045: 2, S0140: 2, H0370: 2, L0483: 2, L0769: 2, L0774: 2, H0521: 2, L0748: 2, L0759: 2, S0114: 1, H0255: 1, H0306: 1, S0046: 1, H0619: 1, S0278: 1, S0280: 1, H0309: 1, T0010: 1, S6028: 1, H0424: 1, H0644: 1, S0036: 1, H0135: 1, H0272: 1, H0412: 1, H0059: 1, H0560: 1, H0561: 1, H0131: 1, H0647: 1, H0649: 1, L0770: 1, L0761: 1, L0776: 1, H0144: 1, H0672: 1, H0576: 1, S3014: 1, S0027: 1, L0749: 1, L0755: 1, S0026: 1, H0665: 1, S0196: 1 and H0506: 1.		

458	HTLGH72	917526	468	33 - 776	1368		AR089: 15, AR061: 11 L0803: 16, S0358: 2, H0031: 2, S0144: 2, L0770: 2, L0804: 2, L0439: 2, L0780: 2, S0116: 1, S0360: 1, H0441: 1, H0431: 1, H0331: 1, H0618: 1, H0544: 1, L0471: 1, H0510: 1, S0318: 1, H0264: 1, L0769: 1, L0783: 1, L0809: 1, L0790: 1, L0438: 1, L0355: 1, L0751: 1, L0779: 1, L0777: 1 and L0758: 1.		
459	HSUAE63	917758	469	896 - 2188	1369	Ser-2 to Gln-22, Pro-94 to His-110, Phe-167 to Ala-172, Leu-261 to Gly-268.	AR061: 2, AR089: 1 L0595: 6, H0069: 4, H0521: 4, L0777: 3, H0663: 2, H0620: 2, H0494: 2, L0646: 2, L0764: 2, L0649: 2, S0152: 2, L0592: 2, T0002: 1, S0040: 1, H0657: 1, H0341: 1, H0661: 1, H0305: 1, H0580: 1, H0645: 1, L0717: 1, H0431: 1, H0587: 1, T0040: 1, H0635: 1, H0575: 1,		

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						His-114 to Ala-125.	L0804: 3, L0748: 3, L0749: 3, S0196: 3, H0530: 2, H0413: 2, L0777: 2, H0686: 1, S0114: 1, H0341: 1, H0638: 1, H0393: 1, H0175: 1, H0071: 1, H0321: 1, H0561: 1, L0769: 1, L0794: 1, L0803: 1, L0805: 1, L0790: 1, L0740: 1, L0747: 1, L0758: 1, S0260: 1 and H0543: 1.		
465	HSKDP26	921366	875	61 - 588	1775	Asp-66 to Gln-71, Ala-84 to Ser-89, His-106 to Ala-118, Tyr-130 to Leu-164, Leu-168 to Val-175.	AR089: 2, AR061: 2 T0074: 3, H0014: 1, S0027: 1 and S0028: 1.		
466	HMTAY52	921948	476	107 - 892	1376	Gln-8 to Ser-16.	AR089: 4, AR061: 2 L0748: 4, L0758: 4, H0457: 3, L0754: 3, S0418: 2, H0253: 2, H0052: 2, S0116: 1, S0356: 1, S0278: 1, H0261: 1, S0222: 1, H0370: 1, H0486: 1, T0082: 1, S0474: 1,		

467	HSDJG01	922453	477	100 - 789	1377	Asp-18 to Leu-23, Asp-29 to Phe-34, His-45 to Asn-52, Gln-64 to Tyr-70, Thr-125 to Arg-131, Glu-133 to His-140, Glu-187 to Ile-195, Asn-224 to Phe-229.	H0057: 1, S0050: 1, H0594: 1, H0213: 1, H0553: 1, H0628: 1, H0617: 1, H0040: 1, H0100: 1, H0494: 1, H0207: 1, H0633: 1, L0763: 1, L0770: 1, L0769: 1, L0796: 1, L0642: 1, L0806: 1, L0805: 1, L0789: 1, L0665: 1, S0052: 1, H0144: 1, H0539: 1, H0518: 1, S0152: 1, L0749: 1, L0750: 1, L0777: 1, L0752: 1, L0601: 1, S0192: 1, S0194: 1 and H0506: 1.			
468	HHEPF30	928000	478	1 - 588	1378	Gly-4 to Gln-10.	AR089: 2, AR061: 2 H0647: 1, H0435: 1, H0518: 1, H0521: 1, S0260: 1 and L0603: 1.	AR089: 15, AR061: 7 L0803: 7, L0759: 6, S0358: 4, L0748: 4, L0754: 4, L0749: 4, L0662: 3, H0413: 2,	15q	

469	HTLAB16	929948	479	1 - 960	1379	AR061: 5, AR089: 1 H0253: 11, L0439: 6, L0794: 4, L0809: 4, L0758: 4, H0618: 3, L0766: 3, H0393: 2, L0803: 2, L0783: 2, L0438: 2, H0341: 1, S0420: 1, S0358: 1, S0362: 1, H0510: 1, H0181: 1, L0769: 1, L0542: 1, L0789: 1, H0187: 1, L0743: 1, L0779: 1 and L0777: 1.	H0529: 2, L0805: 2, H0672: 2, L0758: 2, S0040: 1, L0005: 1, S0360: 1, S0045: 1, H0581: 1, H0015: 1, H0083: 1, S0003: 1, L0142: 1, H0628: 1, H0090: 1, L0769: 1, L0667: 1, L0771: 1, L0790: 1, H0693: 1, H0519: 1, S0378: 1, L0745: 1, L0747: 1, L0777: 1, L0755: 1, L0731: 1, L0485: 1, S0026: 1, H0667: 1, S0242: 1, S0196: 1 and H0543: 1.		
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470	HOHCW42	930431	480	2719 - 1634	1380	Glu-12 to Arg-29, Gly-62 to Phe-69.	AR089: 0, AR061: 0 H0255: 4, H0254: 1, H0638: 1, H0587: 1, S0250: 1, H0617: 1, H0547: 1, H0519: 1, S0032: 1, L0591: 1, H0665: 1 and H0216: 1.		
471	HCHNX75	931615	481	1 - 720	1381		AR089: 2, AR061: 2 L0794: 6, L0758: 6, H0599: 4, L0748: 4, L0759: 4, H0620: 3, L0806: 3, L0809: 3, H0547: 3, L0750: 3, L0752: 3, L0731: 3, H0624: 2, H0484: 2, H0549: 2, H0497: 2, H0486: 2, H0052: 2, H0150: 2, L0471: 2, H0181: 2, S0002: 2, H0529: 2, L0517: 2, L0666: 2, H0520: 2, L0757: 2, S0116: 1, S0045: 1, S0278: 1, H0013: 1, L0738: 1, H0050: 1, H0012: 1, H0622: 1, T0023: 1, H0087: 1, T0067: 1, H0494: 1, S0142: 1, S0344: 1, L0763: 1, L0769: 1, L0768: 1,		

472	HBCBA92	933093	482	1342 - 374	1382	Ser-82 to Gly-87.	L0803: 1, L0650: 1, L0775: 1, L0805: 1, L0776: 1, L0655: 1, L0657: 1, L0658: 1, L0636: 1, L0384: 1, S0052: 1, H0144: 1, S0374: 1, H0519: 1, S0328: 1, H0696: 1, L0439: 1, L0751: 1, L0754: 1 and L0753: 1.		
							AR061: 10, AR089: 6 H0370: 13, H0620: 7, H0556: 4, L0794: 4, L0617: 3, H0251: 3, H0144: 3, L0438: 3, L0439: 3, L0752: 3, H0265: 2, S0358: 2, S0278: 2, H0486: 2, T0042: 2, S0210: 2, L0518: 2, L0666: 2, H0684: 2, H0134: 2, H0555: 2, L0743: 2, T0002: 1, S0134: 1, S0116: 1, H0484: 1, S0420: 1, H0208: 1, H0052: 1, H0012: 1, S0050: 1, H0015: 1, H0594: 1, S6028: 1, H0031: 1, H0598: 1, H0634: 1, H0264: 1.		

									H0100: 1, S0464: 1, S0142: 1, L0640: 1, L0763: 1, L0773: 1, L0662: 1, L0768: 1, L0807: 1, L0382: 1, L0789: 1, H0519: 1, S0330: 1, S3014: 1, L0747: 1, L0758: 1, H0216: 1, H0542: 1 and H0543: 1.			
473	HHFJE1	933110	483	3 - 608	1383	Arg-11 to Arg-16, Gln-34 to Arg-40, Ser-119 to Gln-126, Lys-147 to Gly-157.			AR061: 7, AR089: 4 L0777: 8, H0046: 3, H0263: 2, L0803: 2, L0804: 2, S0360: 1, S0045: 1, H0619: 1, H0642: 1, H0013: 1, H0244: 1, H0039: 1, H0591: 1, L0641: 1, L0766: 1, L0517: 1, H0539: 1 and L0779: 1.			
474	HTXNN68	933670	484	1 - 960	1384	Glu-9 to Gly-14, Pro-28 to Cys-35.			AR061: 5, AR089: 2 H0556: 2, L0770: 2, H0395: 1, S0040: 1, H0657: 1, H0194: 1, H0024: 1, L0667: 1, L0766: 1, H0521: 1, L0740: 1, L0779: 1 and L0588: 1.			
475	HWFW06	933671	485	3 - 533	1385				AR089: 13, AR061: 6 H0556: 2, L0770: 2,			

								H0395: 1, S0040: 1, H0657: 1, H0194: 1, H0024: 1, L0667: 1, L0766: 1, H0521: 1, L0740: 1, L0779: 1 and L0588: 1.			
476	HE2SY77	934771	486	3 - 338	1386	Gln-21 to Trp-32, Lys-81 to Leu-86, Pro-100 to Cys-107.		AR089: 1, AR061: 0 H0624: 1 and S0028: 1.			
477	HSHCO49	934819	487	113 - 766	1387	Ser-1 to Thr-7, Asp-41 to Cys-50, Glu-53 to Gly-61, Asn-89 to Glu-96, Glu-113 to Gln-119.		AR061: 10, AR089: 10 H0519: 1 and S0037: 1.			
478	HMUBI13	937820	488	237 - 899	1388	Phe-10 to Lys-15, Glu-108 to Gly-113, Pro-133 to Lys-142, Glu-152 to Thr-159, Val-196 to Glu-201, Val-216 to Tyr-221.		AR089: 17, AR061: 2 H0521: 5, L0759: 4, S0358: 3, L0757: 3, S0046: 2, H0494: 2, L0662: 2, L0740: 2, H0663: 1, H0638: 1, S0132: 1, H0549: 1, H0586: 1, H0590: 1, H0024: 1, H0083: 1, H0252: 1, H0591: 1, H0551: 1, H0059: 1, H0529: 1, L0389: 1, L0775: 1, L0776: 1, L0665: 1, L0438: 1, H0547: 1, H0435: 1, S0037: 1, L0439: 1,			

479	HBXGL55	938766	489	777 - 1952	1389	<p>Leu-15 to Leu-24, Pro-42 to Asp-54, Ala-123 to Gln-139, Leu-143 to Ala-148, Arg-165 to Asp-170, Arg-176 to Ser-183, Gly-211 to Thr-230, Ser-259 to Asp-268, Gly-309 to Gly-319, Val-326 to Ile-341, Pro-359 to Phe-373, Asp-382 to Asp-392.</p>	<p>L0755: 1, S0434: 1, L0596: 1, L0604: 1, H0667: 1, H0543: 1 and H0422: 1.</p> <p>AR089: 1, AR061: 1 L0769: 8, L0766: 7, L0771: 6, L0806: 6, H0253: 5, H0135: 4, L0741: 4, L0750: 4, H0295: 3, L0774: 3, L0805: 3, L0439: 3, L0751: 3, L0777: 3, L0755: 3, L0731: 3, H0392: 2, L0471: 2, L0770: 2, L0761: 2, L0740: 2, H0624: 1, H0583: 1, H0484: 1, L0617: 1, S0045: 1, S0278: 1, H0438: 1, H0013: 1, H0706: 1, H0618: 1, H0581: 1, H0544: 1, H0046: 1, H0024: 1, T0010: 1, H0286: 1, H0428: 1, H0622: 1, H0124: 1, H0634: 1, H0264: 1, T0042: 1, L0763: 1, L0800: 1, L0794: 1, L0803: 1, L0804: 1, L0650: 1, L0775: 1,</p>		
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								L0659: 1, L0636: 1, L0783: 1, L0789: 1, S0126: 1, H0522: 1, L0779: 1, L0752: 1, L0753: 1 and L0604: 1.			
480	HAFAH26	940254	490	1 - 1053	1390			AR061: 5, AR089: 2 H0643: 2, L0803: 2, S0452: 2, T0049: 1, H0580: 1, H0013: 1, H0156: 1, H0581: 1, H0179: 1, H0271: 1, H0040: 1, S0422: 1, L0369: 1, L0766: 1, L0655: 1, L0607: 1, L0791: 1, H0693: 1, H0670: 1, S0380: 1, H0579: 1, L0777: 1, L0752: 1, S0011: 1 and H0653: 1.			
481	HARMG23	942860	491	1 - 612	1391	Thr-4 to Ser-12.		AR061: 1, AR089: 1 L0777: 3, L0769: 2, S0132: 1, H0592: 1, H0586: 1, H0492: 1, H0004: 1, H0041: 1, H0606: 1, H0038: 1, H0264: 1, S0002: 1, L0371: 1, L0761: 1, L0646: 1, L0794: 1, L0766: 1, L0774: 1, L0664: 1, L0748: 1,			

									L0751: 1, L0750: 1 and L0779: 1.			
482	HOE8MV44	943224	492	2 - 1138	1392	Val-18 to Lys-23, Arg-158 to Trp-167, Ser-176 to Ser-185, Gly-200 to Tyr-207, Pro-216 to Trp-221, Val-257 to Ser-266, Ile-304 to Val-316, Pro-319 to Thr-325, Thr-350 to Ser-358.			AR061: 2, AR089: 2, L0766: 2, L0740: 2, S0356: 1, H0415: 1, H0598: 1, L0803: 1, L0774: 1, L0518: 1, H0539: 1, L0749: 1, L0779: 1 and L0777: 1.			
483	HE9CJ28	949245	493	1506 - 145	1393	Tyr-22 to Gly-40, Glu-56 to Glu-66.			AR061: 1, AR089: 1, H0619: 1, H0549: 1, H0486: 1, H0051: 1, S0250: 1, H0561: 1, S0428: 1, H0144: 1, H0539: 1, L0731: 1, L0592: 1, L0366: 1 and H0667: 1.			
484	HE8AZ89	950713	494	2 - 667	1394				AR089: 1, AR061: 0, H0624: 1, H0013: 1, L0471: 1, S0250: 1, H0038: 1, H0100: 1, T0042: 1, S0150: 1, L0438: 1 and L0592: 1.			
485	HFXKW94	950717	495	190 - 1047	1395	Arg-1 to Gly-6, Thr-74 to Ser-79, Pro-88 to Arg-96.			AR054: 1, AR050: 1, AR089: 1, AR061: 1, S0028: 3, S0222: 2, L0105: 2, S0050: 2, S0390: 2, S0260: 2,			

486	HISAF41	951370	496	1681 - 1226	1396				H0344: 1, H0381: 1, S0282: 1, H0618: 1, S0051: 1, S6028: 1, H0271: 1, H0383: 1, H0264: 1 and S0038: 1. AR061: 1, AR089: 1 L0439: 5, H0529: 3, L0759: 3, S0360: 2, H0024: 2, L0766: 2, L0804: 2, L0779: 2, L0362: 2, H0556: 1, H0656: 1, H0575: 1, H0544: 1, H0015: 1, H0616: 1, H0551: 1, H0412: 1, H0413: 1, L0770: 1, L0662: 1, L0803: 1, L0805: 1, L0655: 1, L0659: 1, L0790: 1, L0665: 1, H0547: 1, H0658: 1, H0539: 1, H0521: 1, L0740: 1, L0745: 1, L0777: 1, L0755: 1, H0445: 1, S0026: 1, H0665: 1 and S0242: 1.		
487	HDPJH11	951371	497	1 - 519	1397	Phe-22 to Thr-27, Lys-71 to Arg-76, Ile-96 to Gly-102, Pro-121 to Trp-133.			AR061: 1, AR089: 1 L0439: 5, H0529: 3, L0759: 3, S0360: 2, H0024: 2, L0766: 2, L0804: 2, L0779: 2,		

488	HLHCP93	950792	498	460 - 218	1398	Lys-18 to Ile-23.	L0362: 2, H0556: 1, H0656: 1, H0575: 1, H0544: 1, H0015: 1, H0616: 1, H0551: 1, H0412: 1, H0413: 1, L0770: 1, L0662: 1, L0803: 1, L0805: 1, L0655: 1, L0659: 1, L0790: 1, L0665: 1, H0547: 1, H0658: 1, H0539: 1, H0521: 1, L0740: 1, L0745: 1, L0777: 1, L0755: 1, H0445: 1, S0026: 1, H0665: 1 and S0242: 1. AR061: 2, AR089: 1 L0439: 5, H0529: 3, L0759: 3, S0360: 2, H0024: 2, L0766: 2, L0803: 2, L0804: 2, L0779: 2, L0362: 2, H0556: 1, H0656: 1, H0575: 1, H0544: 1, H0015: 1, H0616: 1, H0551: 1, H0412: 1, H0413: 1, L0770: 1, L0662: 1, L0805: 1, L0655: 1, L0659: 1, L0790: 1, L0665: 1, H0547: 1, H0658: 1,		
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489	HAIBC14	951372	876	175 - 717	1776	Lys-10 to Gln-20.	AR089: 3, AR061: 3 L0766: 8, L0803: 8, H0046: 7, L0740: 7, L0752: 7, L0754: 6, H0318: 5, H0038: 5, H0551: 5, L0659: 5, S0152: 5, H0624: 4, L0471: 4, S0003: 4, L0666: 4, L0747: 4, L0756: 4, H0422: 4, H0556: 3, S0360: 3, S0045: 3, H0586: 3, H0486: 3, H0590: 3, H0581: 3, H0628: 3, L0662: 3, L0794: 3, L0657: 3, L0809: 3, L0790: 3, L0663: 3, L0664: 3, L0665: 3, H0520: 3, H0658: 3, L0439: 3, L0779: 3, L0777: 3, S0026: 3, H0265: 2, H0657: 2, S0212: 2, H0661: 2, S0418: 2 S0376: 2	10p15	147730	H0539: 1, H0521: 1, L0740: 1, L0745: 1, L0777: 1, L0755: 1, H0445: 1, S0026: 1, H0665: 1 and S0242: 1.
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	H0014: 2, H0266: 2, S0214: 2, H0032: 2, H0068: 2, H0163: 2, H0040: 2, L0598: 2, L0520: 2, L0646: 2, L0771: 2, L0805: 2, L0776: 2, L0655: 2, H0519: 2, H0689: 2, H0660: 2, H0648: 2, H0478: 2, L0731: 2, L0758: 2, H0445: 2, L0595: 2, L0601: 2, S0242: 2, S0040: 1, S0402: 1, S0134: 1, S0116: 1, H0341: 1, H0638: 1, S0354: 1, S0408: 1, S0132: 1, H0619: 1, S0278: 1, H0550: 1, S0222: 1, H0431: 1, H0601: 1, H0587: 1, H0250: 1, L0021: 1, H0575: 1, H0251: 1, H0596: 1, T0110: 1, H0150: 1, H0123: 1, H0050: 1, H0267: 1, S0250: 1, H0328: 1, H0615: 1, H0428: 1, L0483: 1, H0553: 1, H0169: 1, S0036: 1, H0090: 1, H0591: 1, H0616: 1,	
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490	HKAJZ24	951676	500	3 - 827	1400	Gly-8 to Phe-18, His-26 to Phe-41, Glu-56 to Gly-62.	AR089: 1, AR061: 1 S0354: 1, S0358: 1, T0039: 1, H0263: 1.	H0413: 1, H0056: 1, T0041: 1, T0042: 1, H0494: 1, S0150: 1, S0210: 1, H0529: 1, L0640: 1, L0763: 1, L0769: 1, L0638: 1, L0667: 1, L0641: 1, L0773: 1, L0521: 1, L0650: 1, L0774: 1, L0606: 1, L0656: 1, L0634: 1, L0636: 1, L0526: 1, L0518: 1, L0783: 1, L0647: 1, L0789: 1, L0791: 1, H0144: 1, H0698: 1, L0438: 1, H0711: 1, H0435: 1, S0328: 1, H0518: 1, H0521: 1, H0555: 1, H0576: 1, L0356: 1, H0631: 1, S0432: 1, S0028: 1, L0744: 1, L0753: 1, L0759: 1, S0260: 1, L0485: 1, L0362: 1, S0011: 1, S0194: 1, S0196: 1, H0542: 1, H0543: 1 and H0423: 1.		
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491	HWADY95	951731	501	2 - 514	1401	Arg-15 to Asp-21, Arg-59 to Gly-66, Ile-69 to Glu-74, Lys-82 to Tyr-87, Met-95 to Asp-100, Lys-163 to Arg-171.	Phe-114 to Lys-126, Asn-198 to Ser-203, Asn-234 to Ile-242, Glu-264 to Pro-270.	H0494: 1 and S0440: 1.		
492	HCHAG27	952058	502	3 - 812	1402	Ser-50 to Pro-62, Ala-112 to Ser-125.		AR089: 11, AR061: 3 L0748: 3, H0549: 2, H0144: 2, L0021: 1, H0618: 1, H0318: 1, H0581: 1, H0239: 1, H0510: 1, H0264: 1, L0779: 1, L0758: 1, L0596: 1 and S0106: 1.		
493	HPCRA07	952124	503	701 - 15	1403	Glv-27 to Glv-38.		AR089: 3, AR061: 1 L0517: 6, L0751: 6, H0370: 4, L0764: 3, L0666: 3, S0007: 2, L0769: 2, L0646: 2, L0664: 2, H0520: 2, H0484: 1, H0483: 1, S0046: 1, H0644: 1, S0036: 1, H0494: 1, S0440: 1, H0538: 1, L0770: 1, L0772: 1, L0773: 1, L0803: 1, L0657: 1, L0659: 1, L0809: 1, H0690: 1, H0684: 1, H0660: 1, H0627: 1, S0027: 1, L0755: 1 and H0707: 1.		

494	HDMAF23	952729	504	1283 - 219	1404	Thr-67 to Arg-72, Val-87 to Ser-98, Glu-170 to Gly-176, Lys-190 to Asp-200. Arg-6 to Glu-12, Tyr-30 to Thr-35, Val-42 to His-52.	AR089: 6, AR061: 3 S0026: 2, H0638: 1, H0486: 1, H0318: 1, S0214: 1, H0090: 1, T0041: 1, H0494: 1, L0520: 1, L0646: 1, L0666: 1, H0144: 1, S0374: 1, S0146: 1, L0750: 1 and L0485: 1.			
495	HRGBU12	952730	505	3 - 473	1405	Ala-1 to Ser-7, Gln-31 to Leu-46, Arg-49 to Glu-55, Tyr-73 to Asp-79.	AR061: 3, AR089: 3 H0656: 1, H0038: 1, S0210: 1, H0134: 1, H0445: 1 and L0485: 1.			
496	HADFD82	953295	506	16 - 1005	1406	Ala-8 to Pro-23, Ala-25 to Pro-30, Arg-46 to Glu-53.	AR089: 1, AR061: 1 L0766: 7, L0756: 5, H0521: 3, L0777: 3, S0007: 2, H0413: 2, L0761: 2, L0771: 2, L0666: 2, L0748: 2, L0751: 2, H0306: 1, H0402: 1, S0354: 1, S0278: 1, H0441: 1, H0455: 1, H0587: 1, H0486: 1, H0427: 1, H0599: 1, H0581: 1, H0052: 1, H0009: 1.			

497	HCGAF54	954048	507	1 - 636	1407					H0024: 1, H0617: 1, H0040: 1, L0763: 1, L0769: 1, L0646: 1, L0650: 1, L0774: 1, L0775: 1, L0651: 1, L0806: 1, L0655: 1, L0659: 1, L0663: 1, L0665: 1, H0593: 1, H0684: 1, H0436: 1, L0754: 1, L0747: 1, L0758: 1, L0366: 1 and H0543: 1.		
										AR089: 15, AR061: 7 L0747: 6, L0749: 6, L0766: 5, L0775: 5, H0547: 5, L0758: 4, S0358: 3, H0031: 3, L0744: 3, L0759: 3, S0046: 2, L0471: 2, H0616: 2, T0042: 2, L0764: 2, L0774: 2, L0659: 2, L0748: 2, L0740: 2, L0756: 2, L0779: 2, H0668: 2, H0624: 1, H0556: 1, H0661: 1, H0449: 1, H0125: 1, H0351: 1, H0614: 1, H0455: 1, H0438: 1, H0632: 1, H0486: 1, H0590: 1.		

498	HSLGA19	610031	508	1010 - 1654	1408	Asp-5 to Lys-13, Gly-107 to Cys-113, Thr-125 to Leu-131, Lys-146 to Asp-155,	T0048: 1, L0563: 1, H0421: 1, H0596: 1, H0546: 1, H0545: 1, H0046: 1, H0620: 1, S0051: 1, H0510: 1, S6028: 1, H0266: 1, S0334: 1, H0286: 1, S0003: 1, H0591: 1, H0561: 1, S0144: 1, S0344: 1, H0529: 1, L0646: 1, L0650: 1, L0375: 1, L0653: 1, L0776: 1, L0657: 1, L0635: 1, L0792: 1, L0666: 1, L0665: 1, S0374: 1, H0689: 1, H0666: 1, H0539: 1, S0380: 1, H0518: 1, S0152: 1, H0134: 1, H0555: 1, L0743: 1, L0439: 1, L0752: 1, L0755: 1, L0757: 1, S0031: 1, L0592: 1, L0581: 1, L0608: 1, L0595: 1, S0026: 1, H0543: 1 and S0424: 1, AR054: 12, AR061: 2, AR089: 2, AR051: 1 H0381: 1, H0255: 1, S0052: 1 and S0028: 1.		
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					Glu-204 to Gly-214.					
					Leu-29 to Arg-34, Glu-45 to Thr-50, Tyr-67 to Arg-73, Pro-83 to Gln-108, Asp-117 to Val-123, Gln-148 to Glu-155.		1777	2180 - 1323	877	
499	HWWCL36	955759	509	2 - 676	1409					AR089: 7, AR061: 2 H0657: 1, T0023: 1, L0803: 1, H0521: 1, L0731: 1, S0026: 1 and H0423: 1.
500	HD TEN41	955895	510	1 - 1464	1410	Pro-1 to Arg-16.				AR089: 17, AR061: 7 19
501	HSDDDD20	956046	511	1 - 657	1411	Asp-25 to Glu-38, Ala-98 to Phe-104, Gln-152 to Leu-157.				AR089: 1, AR061: 0 S0028: 3, S0001: 2, H0617: 2, L0361: 2, S0356: 1, S0045: 1, H0619: 1, S0278: 1, H0250: 1, H0231: 1, H0181: 1, S0390: 1 and S0031: 1.
502	HDPBL08	959377	512	173 - 979	1412					AR061: 2, AR089: 2 H0616: 4, L0758: 4, H0341: 2, S0358: 2, L0438: 2, L0748: 2, L0779: 2, H0265: 1, S0222: 1, H0431: 1, H0013: 1, H0253: 1, S0010: 1, H0428: 1.

503	HMELJ75	960354	513	114 - 1187	1413	Leu-16 to Phe-21, Thr-69 to Lys-74, Asn-87 to His-92, Thr-126 to Leu-137, Phe-154 to Lys-164, Ala-171 to Asp-178, Ile-192 to Thr-203, Glu-261 to Ser-273.	L0456: 1, H0038: 1, L0151: 1, H0063: 1, H0494: 1, L0767: 1, L0657: 1, S0052: 1, S0152: 1, H0521: 1, L0750: 1, H0707: 1 and H0542: 1.		
							AR061: 4, AR089: 3 S0003: 2, H0591: 2, H0529: 2, L0663: 2, L0750: 2, L0752: 2, L0596: 2, H0171: 1, H0341: 1, H0662: 1, S0420: 1, S0132: 1, H0411: 1, S0222: 1, H0013: 1, H0266: 1, H0428: 1, H0039: 1, H0622: 1, L0483: 1, H0644: 1, H0598: 1, H0040: 1, H0634: 1, L0564: 1, H0280: 1, S0150: 1, L0800: 1, L0764: 1, L0662: 1, L0766: 1, L0529: 1, L0666: 1, H0144: 1, H0660: 1, S0152: 1, H0521: 1, L0779: 1, L0777: 1, L0757: 1, L0758: 1 and H0543: 1.		
504	HLTCU08	960951	514	27 - 686	1414	Thr-1 to Asn-17.	AR061: 4, AR089: 3		

Lys-38 to Glu-45, Tyr-74 to Arg-79, Ala-90 to Val-95, Phe-124 to Gln-142, Val-180 to His-189.	L0777: 13, L0740: 8, L0759: 5, L0608: 5, H0031: 4, H0042: 3, L0771: 3, L0665: 3, L0748: 3, L0439: 3, L0754: 3, H0024: 2, L0769: 2, L0794: 2, L0766: 2, L0806: 2, L0790: 2, H0521: 2, L0750: 2, L0756: 2, L0758: 2, L0592: 2, H0556: 1, H0159: 1, T0049: 1, H0657: 1, S0007: 1, S0046: 1, H0619: 1, S0222: 1, H0574: 1, H0486: 1, S0346: 1, H0318: 1, H0581: 1, H0052: 1, H0327: 1, H0051: 1, T0010: 1, H0039: 1, L0483: 1, L0143: 1, H0032: 1, H0673: 1, H0090: 1, H0038: 1, T0067: 1, S0038: 1, H0529: 1, L0640: 1, L0763: 1, L0639: 1, L0667: 1, L0764: 1, L0662: 1, L0768: 1, L0523: 1, L0657: 1, L0659: 1, H0144: 1, H0659: 1, H0658: 1.
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									S0328: 1, H0539: 1, S0378: 1, S0028: 1, L0747: 1, L0752: 1, L0753: 1, L0755: 1, L0731: 1, L0596: 1, L0595: 1, H0543: 1 and S0412: 1.			
505	HTOHK41	960955	515	1065 - 151	1415	His-10 to Pro-16.			AR089: 20, AR061: 6 H0265: 2, S0040: 1, H0250: 1 and H0264: 1.			
506	HTKAA03	961002	516	2 - 202	1416	Asn-1 to Thr-9, Thr-40 to Asp-51.			S0300: 1, S0028: 1 and T0047: 1.			
507	HMSGF27	962420	517	3 - 332	1417	Arg-1 to Asp-6, Ala-47 to Pro-58.			AR089: 12, AR061: 8 L0766: 4, H0052: 3, L0662: 3, L0776: 3, L0666: 3, L0665: 3, H0521: 3, H0438: 2, H0581: 2, H0263: 2, H0494: 2, L0763: 2, L0770: 2, L0769: 2, L0649: 2, L0664: 2, L0748: 2, L0439: 2, L0747: 2, S0436: 2, H0265: 1, H0556: 1, S0040: 1, S0444: 1, S0278: 1, H0415: 1, H0403: 1, H0643: 1, S0280: 1, H0575: 1, H0194: 1, H0309: 1, H0545: 1 H0046: 1			

508	HHFLM17	963511	518	3 - 470	1418	Pro-45 to Pro-52, Asn-79 to Ala-84, Gly-124 to Ser-129.	AR089: 2, AR061: 1 H0619: 1, H0529: 1, L0375: 1 and H0543: 1.	L0157: 1, H0375: 1, L0483: 1, H0553: 1, H0412: 1, H0646: 1, S0002: 1, L0796: 1, L0644: 1, L0764: 1, L0774: 1, L0376: 1, L0806: 1, L0654: 1, L0659: 1, L0383: 1, S0126: 1, H0684: 1, H0435: 1, H0478: 1, S0028: 1, L0751: 1, L0754: 1, L0749: 1, L0750: 1, L0779: 1, L0759: 1, H0543: 1 and H0423: 1.	1p32-p34	120950, 120960, 130500, 133200, 138140, 168360, 171760, 171760, 176100, 176100, 178300, 187040, 230000, 255800, 600101,
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									600650, 600650, 600722, 600722
509	HLICLI0	964035	519	3 - 761	1419	Glu-121 to Lys-126, Pro-148 to Lys-154, Thr-181 to Asp-187, Val-208 to Asp-214, Pro-223 to Phe-231, Glu-239 to Lys-245.		AR089: 99, AR061: 59 H0393: 1, S0278: 1, H0643: 1, H0196: 1, H0231: 1, H0200: 1, H0355: 1, S0037: 1, S0027: 1, H0445: 1 and H0423: 1.	
510	HCUAZ04	965585	520	546 - 214	1420	Lys-6 to Phe-11.		AR089: 1, AR061: 0 L0769: 8, L0748: 4, L0759: 4, H0038: 3, L0750: 3, L0755: 3, H0556: 2, S0356: 2, H0574: 2, L0163: 2, L0766: 2, L0776: 2, L0663: 2, L0752: 2, L0731: 2, L0599: 2, H0255: 1, H0306: 1, H0125: 1, S0376: 1, H0580: 1, H0455: 1, H0497: 1, H0331: 1, L0021: 1, H0004: 1, H0618: 1, S0010: 1, H0546: 1, H0545: 1, H0123: 1, H0081: 1, H0578: 1, H0051: 1, H0510: 1, H0188: 1,	

511	HE2SB11	965611	521	103 - 441	1421					H0617: 1, H0032: 1, H0169: 1, T0042: 1, L0475: 1, H0560: 1, H0132: 1, L0770: 1, L0372: 1, L0764: 1, L0771: 1, L0774: 1, L0783: 1, L0665: 1, L0438: 1, S0028: 1, L0439: 1, L0740: 1, L0786: 1, L0779: 1, L0757: 1, L0758: 1, L0588: 1, L0605: 1, S0192: 1 and S0276: 1.		
512	HCFLJ17	954723	522	1 - 423	1422	Thr-2 to Gln-9, Glu-19 to Glu-29, Glu-43 to Ser-67.				AR089: 4, AR061: 2 L0758: 7, L0362: 5, S0358: 4, L0766: 4, L0754: 4, H0318: 3, H0551: 3, H0529: 3, L0803: 3, H0519: 3, L0750: 3, L0777: 3, H0423: 3, H0650: 2, H0369: 2, H0575: 2, T0110: 2 S0003: 2		

								H0658: 1, H0660: 1, H0521: 1, H0555: 1, S0028: 1, L0742: 1, L0756: 1, S0192: 1, S0242: 1, S0194: 1 and S0276: 1.		
513	HLICJ19	966969	523	1 - 321	1778	Glu-14 to Glu-24, Glu-38 to Ser-62, Ala-177 to Ala-198, Glu-235 to Arg-240, His-257 to Lys-374.		AR061: 27, AR089: 6 S0040: 1, H0355: 1, H0328: 1, L0374: 1, L0794: 1, L0766: 1 and S3014: 1.		
514	HDPSM18	967483	524	1 - 315	1424	Thr-27 to Asn-33.		AR061: 2, AR089: 1 H0556: 1, S0212: 1, H0373: 1, H0553: 1, H0063: 1, H0477: 1, S0152: 1, H0521: 1 and S0026: 1.		
515	HMAKJ82	967593	525	1 - 501	1425	Thr-3 to Gly-13, Trp-35 to Glu-40, Ser-51 to His-56.		AR089: 8, AR061: 8 L0794: 6, L0758: 6, H0599: 4, L0748: 4, L0759: 4, H0620: 3, L0806: 3, L0809: 3, H0547: 3, L0750: 3, L0752: 3, L0731: 3, H0624: 2, H0484: 2,		

516	HFPIX37	971428	526	1 - 507	1426	Pro-75 to Asp-84, Pro-92 to Pro-101, Arg-161 to Trp-167.	H0549: 2, H0497: 2, H0486: 2, H0052: 2, H0150: 2, L0471: 2, H0181: 2, S0002: 2, H0529: 2, L0517: 2, L0666: 2, H0520: 2, L0757: 2, S0116: 1, S0045: 1, S0278: 1, H0013: 1, L0738: 1, H0050: 1, H0012: 1, H0622: 1, T0023: 1, H0087: 1, T0067: 1, H0494: 1, S0142: 1, S0344: 1, L0763: 1, L0769: 1, L0768: 1, L0803: 1, L0650: 1, L0775: 1, L0805: 1, L0776: 1, L0655: 1, L0657: 1, L0658: 1, L0636: 1, L0384: 1, S0052: 1, H0144: 1, S0374: 1, H0519: 1, S0328: 1, H0696: 1, L0439: 1, L0751: 1, L0754: 1 and L0753: 1.		
							AR089: 4, AR061: 1, H0583: 1, H0662: 1, S0222: 1, S0049: 1, H0272: 1, H0670: 1, H0521: 1, H0555: 1 and		

517	HHEKP47	974402	527	75 - 527	1427	Ser-1 to Thr-7, Pro-15 to Asp-22, Glu-138 to Ser-143.	S0436: 1. AR089: 1, AR061: 1 H0542: 6, H0637: 3, H0580: 3, H0555: 2, H0592: 1, H0586: 1, H0544: 1, H0546: 1, H0545: 1, H0529: 1, H0703: 1, H0593: 1, H0521: 1 and H0543: 1.	1q32	114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580, 145260, 150310, 150310, 179820, 191045, 600105, 600759, 601494, 601975
518	HTPDV62	418671	528	2 - 358	1428		AR061: 7, AR089: 4 H0663: 2, H0069: 2, H0634: 2, H0635: 1, H0618: 1 and H0039: 1.	1q32-q41	114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580,

										145260, 150310, 150310, 179820, 191045, 276901, 600105, 600332, 600759, 601494, 601744, 601975
519	HUSAJ73	567234	529	1 - 201	1429				AR061: 8, AR089: 7 S0045: 1, S0046: 1, H0574: 1 and H0268: 1.	
520	HSKCIJ76	747380	530	115 - 414	1430	Phe-12 to Thr-17.			AR061: 6, AR089: 5	
521	HCEOX38	881200	531	3 - 386	1431	Met-1 to Ile-23, Asp-85 to Asp-91.			AR089: 2, AR061: 1 H0052: 1 and H0435: 1.	100710, 138190, 231200, 254210, 262850, 271900, 600179, 600977, 601202, 601777
522	HFICR59	911317	532	2 - 721	1432	Ser-2 to Lys-7, Thr-73 to Ala-86, Gly-108 to Asn-113,			AR089: 1, AR061: 0 L0794: 6, L0598: 2, L0803: 2, L0748: 2,	

523	HPDVO67	911405	533	1 - 645	1433	Ser-184 to Val-190.	S0040: 1, S0046: 1, H0431: 1, H0318: 1, L0766: 1, L0606: 1, L0749: 1, L0758: 1 and S0192: 1.	19p13.3	108725, 120700, 133171, 136836, 145981, 147141, 164953, 188070, 600957, 601238, 601846, 602216, 602477
524	H2LAD53	952181	534	1 - 360	1434	Glu-1 to Tyr-10, Lys-37 to Leu-44, Glu-66 to Leu-75, Glu-80 to His-91.	AR089: 2, AR061: 2 L0751: 10, L0666: 4, L0743: 3, H0253: 2, H0622: 2, H0670: 2, L0779: 2, H0685: 1, H0181: 1, S0382: 1, L0372: 1, L0646: 1, L0773: 1, L0767: 1, L0768: 1, L0657: 1, L0665: 1, S0374: 1, H0658: 1, L0749: 1, L0777: 1, L0758: 1 and L0593: 1.		
						Glu-1 to Asp-6, Thr-11 to Glu-20, Val-61 to Pro-67, Ala-128 to Leu-136, Glu-141 to Ser-147, Arg-173 to Pro-179.	AR089: 18, AR061: 13 S0136: 47, L0769: 10, L0439: 7, L0750: 7, H0620: 5, L0776: 5, L0740: 5, L0752: 5, L0509: 4, L0809: 4, L0666: 4, L0748: 4, H0624: 3, H0265: 3, H0341: 3, S0418: 3, L0717: 3, L0764: 3, L0659: 3, L0755: 3, S0026: 3, H0556: 2,		

S0356: 2, S0358: 2,
S0360: 2, H0574: 2,
T0060: 2, S0010: 2,
H0046: 2, H0510: 2,
H0032: 2, H0169: 2,
H0413: 2, H0646: 2,
L0646: 2, L0766: 2,
L0803: 2, L0805: 2,
L0665: 2, S0374: 2,
H0519: 2, H0659: 2,
H0648: 2, S0328: 2,
S0378: 2, S0380: 2,
S03014: 2, L0756: 2,
L0777: 2, L0731: 2,
L0758: 2, L0588: 2,
L0589: 2, L0594: 2,
H0543: 2, H0171: 1,
S0040: 1, T0049: 1,
L0002: 1, H0657: 1,
H0346: 1, H0255: 1,
H0664: 1, H0305: 1,
H0589: 1, S0376: 1,
H0675: 1, S0045: 1,
S0046: 1, H0586: 1,
H0587: 1, H0333: 1,
H0642: 1, H0331: 1,
H0632: 1, H0486: 1,
H0013: 1, H0427: 1,
L0021: 1, H0575: 1,
H0590: 1, S0182: 1,
H0085: 1, H0596: 1.

	H0546: 1, L0157: 1, H0572: 1, H0571: 1, H0024: 1, L0695: 1, H0373: 1, L0163: 1, S6028: 1, H0266: 1, S0003: 1, H0252: 1, T0006: 1, H0166: 1, H0674: 1, S0364: 1, L0455: 1, H0124: 1, H0598: 1, H0400: 1, H0135: 1, H0163: 1, H0038: 1, H0616: 1, H0551: 1, T0067: 1, H0100: 1, T0041: 1, S0448: 1, S0450: 1, H0509: 1, H0647: 1, S0208: 1, L0770: 1, L0637: 1, L0772: 1, L0372: 1, L0800: 1, L0374: 1, L0662: 1, L0388: 1, L0774: 1, L0775: 1, L0375: 1, L0653: 1, L0628: 1, L0513: 1, L0526: 1, L0518: 1, L0382: 1, L0663: 1, L0664: 1, L0565: 1, L0438: 1, H0660: 1, H0666: 1, S0044: 1, S0037: 1, S0206: 1, L0747: 1, L0780: 1, L0753: 1,
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									L0757: 1, L0759: 1, H0445: 1, L0592: 1, L0485: 1, L0608: 1, L0603: 1, L0097: 1 and S0446: 1.		
		972357	879	672 - 887	1779	Glu-42 to Val-48, Glu-63 to Asp-72.					
		972358	880	848 - 645	1780						
525	HETLM90	954181	535	1 - 771	1435	Ile-29 to Gln-36.			AR061: 7, AR089: 6 S0404: 7, L0754: 4, L0731: 4, H0046: 3, L0662: 3, H0519: 2, L0439: 2, L0756: 2, L0758: 2, S0242: 2, H0171: 1, L0021: 1, H0194: 1, H0251: 1, L0471: 1, H0057: 1, S6028: 1, H0615: 1, H0063: 1, H0494: 1, L0598: 1, L0520: 1, L0646: 1, L0641: 1, L0794: 1, L0766: 1, L0803: 1, L0666: 1, H0144: 1, S0374: 1, H0690: 1, H0539: 1, S0380: 1, H0696: 1, H0436: 1, L0740: 1, L0755: 1 and S0031: 1.		
526	HCE5E94	969287	536	270 - 410	1436	Ser-1 to Gly-8, Lys-14 to Pro-21,			AR089: 1 H0619: 5, L0439: 5,		

Ser-25 to Cys-33, Pro-37 to Gly-44.						L0770: 4, T0049: 2, H0052: 2, H0544: 2, H0268: 2, L0748: 2, L0740: 2, L0749: 2, L0756: 2, L0759: 2, H0624: 1, H0170: 1, H0662: 1, H0306: 1, S0420: 1, S0376: 1, S0045: 1, S0132: 1, S0278: 1, H0587: 1, H0574: 1, S0280: 1, H0599: 1, H0546: 1, H0124: 1, H0135: 1, H0163: 1, H0551: 1, H0264: 1, H0269: 1, H0413: 1, H0646: 1, S0208: 1, L0631: 1, L0761: 1, L0764: 1, L0662: 1, L0766: 1, L0803: 1, L0806: 1, L0805: 1, L0653: 1, L0659: 1, L0809: 1, L0666: 1, L0665: 1, L0438: 1, H0670: 1, H0518: 1, H0436: 1, S0037: 1, S0027: 1, L0743: 1, L0750: 1, L0777: 1, L0758: 1, H0595: 1, L0601: 1, H0423: 1 and H0506: 1.
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		969299	881	889 - 1386	1781	Pro-23 to Trp-28, Pro-35 to Lys-41, Gln-101 to Glu-110, Glu-122 to Gly-129.			
		971074	882	3 - 1097	1782				
527	HFXCUC55	499457	537	183 - 1	1437	Lys-32 to Lys-51.	AR061: 1, AR089: 0 S0001: 1 and H0150: 1.		
528	HEPBV24	513261	538	73 - 393	1438	Glu-24 to His-33.	AR089: 619, AR061: 539 S0001: 1 and H0150: 1.		
529	HFRAU96	527840	539	13 - 363	1439		AR089: 1, AR061: 0 S0050: 1 and S0044: 1.		
530	HTLBD23	527944	540	3 - 413	1440	His-1 to Gly-6, Ser-13 to Phe-18.	AR061: 8, AR089: 3 H0013: 4, H0617: 2, S0428: 2, S0032: 2, S0001: 1, T0074: 1, H0253: 1, H0318: 1, S0050: 1, L0456: 1, H0268: 1 and S0390: 1.		
531	HCEBM51	536558	541	3 - 470	1441	Asp-17 to Ala-25.	AR089: 2, AR061: 1 H0040: 3, H0087: 3, H0052: 2, L0747: 2, L0601: 2, S0010: 1, H0327: 1, S0051: 1, H0181: 1, L0741: 1, L0745: 1, L0753: 1 and S0106: 1.		
532	HSLFF79	609838	542	64 - 741	1442	Phe-132 to Gln-137, Arg-209 to Gly-220.	AR089: 1, AR061: 0 S0028: 2 and S0300: 1.		
		961693	883	866 - 174	1783	Phe-137 to Gln-142,			

533	HKTAB71	661483	543	3 - 398	1443	Arg-214 to Gly-225. Asp-47 to Asn-53, Pro-118 to Thr-132.	AR089: 14, AR061: 4 L0774: 3, L0749: 2, H0239: 1, L0803: 1 and S0378: 1.		
534	HSDIF25	678003	544	36 - 446	1444		AR089: 1, AR061: 0 S0390: 1 and S0260: 1.		
535	HNHHW82	684342	545	3 - 284	1445	Ala-1 to Arg-10, His-15 to Asp-20.	AR089: 11, AR061: 4 S0053: 2 and S0050: 1.		
536	HFATN41	712097	546	259 - 717	1446	Gly-37 to Asp-50.	AR061: 3, AR089: 2 S0300: 1 and H0031: 1.		
537	HHEFFG80	733387	547	2 - 478	1447		AR089: 15, AR061: 6 H0050: 1 and H0522: 1.		
538	HSDEFF73	761657	548	3 - 515	1448		AR061: 139, AR089: 37 S0028: 1 and S0031: 1.		
539	HTLBH79	774422	549	3 - 572	1449		AR054: 22, AR051: 20, AR089: 4, AR061: 3, AR050: 2 L0439: 2, S0358: 1, H0486: 1, H0253: 1, H0593: 1 and H0522: 1.		
		797621	884	715 - 263	1784				
		971837	885	307 - 828	1785	Glu-11 to Arg-17.			
540	HBWCD80	777346	550	2 - 868	1450	Leu-26 to Ser-31, Pro-68 to Lys-82.	AR089: 1, AR061: 0		
541	HSDKI89	786812	551	3 - 521	1451	Asp-8 to Gly-26, Tyr-43 to Ser-49, Ser-137 to Lys-148.	AR061: 1, AR089: 1		

542	HIBDA29	810879	552	2 - 403	1452		AR089: 1, AR061: 1 T0010: 2, H0172: 1, H0100: 1, L0769: 1, L0792: 1, L0745: 1 and L0756: 1.		
543	HLDQU68	825558	553	1 - 429	1453	Trp-10 to Gly-16, Asp-30 to Ala-39, Glu-72 to Ser-87, Asn-112 to Trp-124.	AR061: 9, AR089: 2 H0351: 1 and H0510: 1.		
544	HMUAS41	827510	554	2 - 385	1454	Asn-37 to Gln-42, Thr-56 to Leu-62, Asn-68 to Lys-74.	AR089: 4, AR061: 2 S0007: 3, S0354: 2, H0529: 2, H0645: 1, H0052: 1 and H0039: 1.		
545	HTXOH20	837509	555	1 - 426	1455	Glu-1 to Gly-9, Asn-17 to Lys-22, Asp-30 to Phe-36, Lys-43 to Glu-49, Pro-133 to Lys-142.	AR061: 3, AR089: 2		
546	HSLFG13	847314	556	154 - 705	1456		AR089: 1, AR061: 0 S0028: 1 and S3018: 1.		
547	HDAAS21	850577	557	2 - 724	1457	Leu-26 to Cys-37, Cys-127 to Glu-132.	AR061: 158, AR089: 3 H0497: 2, L0766: 2, L0777: 2, H0589: 1, L0627: 1, L0779: 1, L0759: 1, L0604: 1 and H0506: 1.		
548	HARMH10	852701	558	736 - 146	1458	Gln-1 to Pro-6.	AR089: 9, AR061: 3 H0592: 1, S0150: 1, H0521: 1 and L0740: 1.		
549	HSDAI07	859237	559	72 - 623	1459	Ser-10 to Cys-16.	AR089: 1, AR061: 0		

550	HLDQU41	864996	560	1 - 504	1460	Glu-62 to Arg-69, Ser-140 to Thr-146.	S0126: 2, S0031: 2 and S0045: 1. AR061: 765, AR089: 3 L0803: 10, L0439: 5, L0617: 2, L0774: 2, L0438: 2, L0742: 2, L0747: 2, H0574: 1, H0510: 1, H0038: 1, L0804: 1, L0775: 1, L0789: 1 and L0581: 1.		
551	HABU06	864997	561	20 - 937	1461	Ser-29 to Ser-38, Ser-63 to Thr-69, Glu-90 to Asp-97; Phe-127 to Glu-135, His-215 to His-229, Asp-245 to Asp-257.	AR089: 4, AR061: 2 H0359: 1 and H0561: 1.		
552	HSLDO63	866332	562	3 - 521	1462	Trp-14 to Asn-30, Val-44 to Leu-50, Leu-116 to Tyr-121, Ser-164 to Thr-172.	AR061: 4, AR089: 4 S0028: 1 and H0542: 1.		
553	HNHAG26	866694	563	251 - 880	1463		AR061: 7, AR089: 2		
554	HGBGC61	867065	564	449 - 3	1464		AR089: 1, AR061: 0 H0416: 1, H0181: 1, H0617: 1 and H0316: 1.		
555	HMAEM27	870252	565	3 - 716	1465		AR089: 88, AR061: 44 H0494: 1, S0144: 1, L0749: 1, L0605: 1 and L0593: 1.		
556	HEBCK42	875541	566	313 - 74	1466	Glu-1 to Lys-6,	AR089: 26, AR061: 9 10q11.1-q24	157640,	

						Lys-15 to Asp-25.		H0031: 4, S0007: 1 and L0748: 1.		174900, 180250, 186770, 188550, 236730, 271245, 278000, 278000, 600095, 600512, 600835, 601107, 601130, 602082
557	HELNF03	881180	567	323 - 736	1467	Arg-8 to Met-21, Ser-32 to Ala-37.		AR089: 2, AR061: 1 H0381: 2, H0617: 2, S0045: 1 and S0044: 1.		
558	HKINF95	882308	568	1 - 270	1468			AR061: 399, AR089: 71 H0069: 1, H0399: 1, S0428: 1, H0698: 1 and H0521: 1.		
559	HTLHE85	883263	569	1 - 663	1469	Tyr-20 to Trp-25, Leu-39 to Ser-44, Asp-62 to Thr-79.		AR089: 18, AR061: 13 H0618: 2, H0013: 1 and H0424: 1.		
560	HTEOE72	886412	570	1 - 675	1470	Thr-2 to Ser-9, Pro-23 to Arg-30, Pro-44 to Arg-49, Ser-62 to Pro-73, Phe-150 to Lys-155,		AR050: 14, AR051: 12, AR054: 10, AR061: 6, AR089: 3 H0038: 2, H0616: 1, S0152: 1 and S0242: 1.		

561	HELENI3	907599	571	318 - 659	1471	Asp-164 to Glu-169, Leu-191 to Val-198. Glu-13 to Trp-22, Gln-60 to Lys-65.	AR089: 1, AR061: 1 S0045: 1, S0144: 1, S0028: 1 and S0260: 1.		
562	HFIJE03	914882	572	1762 - 1052	1472	Pro-11 to Asn-16, Lys-67 to His-75, Gly-145 to Trp-152, Glu-171 to Arg-176, Met-220 to Glu-230.	AR089: 15, AR061: 6 L0766: 3, L0596: 2, S0134: 1, H0327: 1, T0010: 1, H0616: 1, H0551: 1, L0363: 1, L0783: 1, H0520: 1, S0152: 1, H0555: 1, L0748: 1, L0439: 1, S0194: 1, H0423: 1 and H0506: 1.		
563	HABGE01	915743	573	2 - 1276	1473	Leu-39 to Lys-47, Gly-67 to Thr-76, Thr-86 to Thr-96.	AR089: 0, AR061: 0		
564	HWLKM02	917409	574	1012 - 11	1474	Ala-2 to Glu-7, Leu-9 to Pro-17, Pro-30 to Glu-41, Gln-50 to Gly-56.	AR089: 3, AR061: 2 S0358: 5, H0617: 4, H0559: 3, L0804: 2, L0805: 2, H0657: 1, S0007: 1, H0455: 1, H0618: 1, H0546: 1, H0545: 1, H0488: 1, L0637: 1, L0775: 1, L0809: 1, L0789: 1, L0438: 1, L0439: 1, L0752: 1 and L0757: 1.		
565	HOVERI3	917564	575	122 - 904	1475	Gly-27 to Ala-33	AR089: 5, AR061: 2		

						Leu-45 to Asn-53, Lys-86 to Ala-91, Ala-132 to Arg-137, Lys-174 to Phe-183, Gln-200 to Pro-207, Asp-251 to Gln-256.	L0779: 4, H0428: 3, L0773: 2, L0662: 2, L0659: 2, L0602: 2, L0777: 2, L0596: 2, L0608: 2, H0170: 1, H0580: 1, S0045: 1, T0048: 1, H0052: 1, L0471: 1, H0628: 1, L0770: 1, L0761: 1, L0805: 1, L0653: 1, L0657: 1, L0512: 1, H0682: 1, H0672: 1, L0748: 1, L0740: 1, L0749: 1, L0757: 1, S0031: 1, H0543: 1 and H0677: 1.		
566	HE8UB94	920288	576	187 - 561	1476	Gly-16 to Glu-21.	AR061: 2, AR089: 1 L0750: 7, L0777: 7, H0013: 6, L0805: 6, H0521: 4, L0596: 4, H0014: 3, L0756: 3, H0170: 2, S0360: 2, H0051: 2, H0622: 2, H0090: 2, S0002: 2, H0529: 2, L0776: 2, L0655: 2, L0606: 2, H0520: 2, H0547: 2, L0755: 2, L0759: 2, L0485: 2, L0604: 2, S0026: 2, H0171: 1.		.

567	HTHJDJ23	921274	577	1368 - 1739	1477	Ser-25 to Lys-30.	S0116: 1, H0341: 1, S0045: 1, S0222: 1, S6014: 1, H0431: 1, H0587: 1, H0331: 1, H0486: 1, H0156: 1, L0021: 1, S0049: 1, H0309: 1, H0046: 1, H0086: 1, H0123: 1, S0388: 1, H0687: 1, H0111: 1, H0598: 1, H0616: 1, H0264: 1, H0561: 1, H0538: 1, S0426: 1, L0637: 1, L0646: 1, L0764: 1, L0521: 1, L0364: 1, L0803: 1, L0775: 1, L0527: 1, L0666: 1, H0144: 1, S0374: 1, H0519: 1, H0690: 1, H0435: 1, H0648: 1, S0330: 1, S0152: 1, L0748: 1, L0751: 1, L0745: 1, L0747: 1, L0731: 1, L0758: 1, H0423: 1, H0422: 1 and S0462: 1.		
							AR051: 27, AR050: 26, AR054: 22, AR061: 4, AR089: 4 S0358: 1 H0266: 1		

568	HWHPB72	922580	578	454 - 768	1478				H0687: 1, H0063: 1 and L0749: 1. AR089: 4, AR061: 3 L0438: 3, S0007: 2, S0134: 1, H0587: 1, H0497: 1, H0123: 1, H0428: 1, H0039: 1, H0551: 1, H0623: 1, H0509: 1, H0435: 1, H0518: 1, L0748: 1 and L0759: 1.		
569	HSQFX64	922581	579	1 - 324	1479				AR089: 11, AR061: 6		
570	HDABB84	922582	580	3 - 1760	1480				AR089: 9, AR061: 1 H0056: 2, H0059: 2, L0800: 2, L0663: 2, L0602: 2, L0747: 2, L0588: 2, L0591: 2, L0592: 2, L0599: 2, H0686: 1, S0360: 1, S0132: 1, H0497: 1, S0280: 1, H0042: 1, S0036: 1, H0634: 1, L0351: 1, H0560: 1, S0448: 1, H0509: 1, H0529: 1, L0764: 1, L0794: 1, L0774: 1, L0775: 1, L0375: 1, L0809: 1, L0666: 1, S0374: 1, L0438: 1,		

								H0547: 1, H0435: 1, H0651: 1, S0380: 1, L0748: 1, L0749: 1, L0779: 1, L0752: 1, L0731: 1, L0759: 1, H0543: 1, H0423: 1 and H0506: 1.			
571	HLHFN83	924110	581	3 - 263	1481			AR089: 14, AR061: 8 H0510: 2, L0595: 2, H0657: 1, H0580: 1, H0619: 1, H0357: 1, H0632: 1, H0013: 1, H0024: 1, H0578: 1, H0591: 1, H0509: 1, L0769: 1, L0804: 1, L0805: 1, L0776: 1, H0521: 1, H0555: 1, L0740: 1, L0749: 1 and H0423: 1.			
572	HPCRR26	926401	582	870 - 253	1482	Asp-10 to Thr-15, Leu-19 to Arg-26, Gly-120 to Asn-125, Lys-131 to Ser-139, Gly-169 to Lys-174, Glu-199 to Met-205.		AR089: 1, AR061: 0			
573	HCMSD61	927475	583	66 - 959	1483	Arg-17 to Asn-23, Arg-90 to Gly-95, Leu-114 to Glu-121, Pro-153 to Asp-158, Thr-288 to Lys-295.		AR061: 6, AR089: 5 L0775: 5, H0486: 3, H0648: 3, L0748: 3, L0758: 3, H0657: 2, S0358: 2, H0370: 2,			

									H0331: 2, H0040: 2, H0616: 2, S0152: 2, L0754: 2, L0747: 2, L0759: 2, S0192: 2, H0170: 1, H0664: 1, S0356: 1, S0222: 1, H0575: 1, H0196: 1, H0014: 1, H0373: 1, H0039: 1, H0622: 1, T0023: 1, L0483: 1, H0644: 1, L0142: 1, H0674: 1, H0090: 1, H0059: 1, S0422: 1, L0772: 1, L0768: 1, L0766: 1, L0774: 1, L0655: 1, H0547: 1, H0435: 1, H0659: 1, H0521: 1, S0027: 1, L0740: 1, L0756: 1, H0445: 1, L0593: 1, H0668: 1, L0462: 1 and H0352: 1.					
574	HCEEC58	933866	584	1 - 327	1484				AR089: 110, AR061: 37 S0007: 3, S0354: 2, H0529: 2, H0645: 1, H0052: 1 and H0039: 1. AR061: 4, AR089: 3					
575	HSYAD06	935334	585	1 - 765	1485									
576	HUSID53	943374	586	2 - 994	1486	Arg-1 to Glu-6,			AR089: 1, AR061: 1					

577	HRGDE77	948737	587	2 - 1051	1487	Lys-25 to Arg-32, Gly-53 to Asn-61, Asn-116 to Glu-121, Thr-194 to Thr-199, Asn-209 to Thr-217. Arg-20 to Leu-28, Phe-57 to Arg-79.	H0522: 2, H0052: 1, H0412: 1, L0794: 1, L0803: 1, H0651: 1, H0521: 1, L0748: 1, L0749: 1 and L0752: 1. AR089: 12, AR061: 8 L0751: 10, L0748: 9, S0222: 6, L0438: 4, L0747: 4, S0356: 3, H0040: 3, S0344: 3, L0766: 3, L0809: 3, L0665: 3, S0380: 3, L0758: 3, H0624: 2, S0360: 2, S0010: 2, H0014: 2, H0399: 2, H0622: 2, S0038: 2, S0144: 2, S0002: 2, L0770: 2, L0803: 2, H0666: 2, L0439: 2, L0749: 2, L0596: 2, L0595: 2, S0218: 1, S0400: 1, H0483: 1, S0045: 1, H0619: 1, H0393: 1, S0278: 1, H0250: 1, H0618: 1, H0253: 1, H0052: 1, H0457: 1, H0123: 1, H0242: 1, H0266: 1, H0687: 1, H0264: 1, H0102: 1 H0641: 1		
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578	HEGAU68	950009	588	239 - 520	1488			H0646: 1, L0763: 1, L0771: 1, L0794: 1, L0804: 1, L0776: 1, L0807: 1, L0788: 1, L0664: 1, S0052: 1, H0144: 1, H0547: 1, H0689: 1, H0659: 1, H0648: 1, H0521: 1, H0696: 1, H0134: 1, L0779: 1 and L0605: 1. AR089: 11, AR061: 4 L0744: 9, L0731: 8, L0439: 7, H0144: 5, L0749: 5, L0748: 4, L0745: 4, L0758: 4, S0040: 3, H0013: 3, H0038: 3, L0769: 3, L0773: 3, L0755: 3, H0306: 2, S0356: 2, S0358: 2, H0550: 2, H0392: 2, S0280: 2, H0620: 2, T0003: 2, H0598: 2, S0036: 2, H0623: 2, S0344: 2, S0002: 2, L0662: 2, L0768: 2, L0561: 2, L0775: 2, L0776: 2, L0527: 2, L0783: 2, L0438: 2, S0126: 2, H0539: 2, S0152: 2.		
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	H0521: 2, S3014: 2, L0754: 2, L0747: 2, L0780: 2, L0752: 2, L0757: 2, L0591: 2, L0608: 2, L0362: 2, L0361: 2, L0601: 2, L0603: 2, H0170: 1, H0265: 1, H0556: 1, T0002: 1, S0114: 1, L0427: 1, S0116: 1, S0282: 1, H0402: 1, S0420: 1, S0354: 1, S0376: 1, S0360: 1, H0208: 1, S0045: 1, S0132: 1, S0278: 1, H0549: 1, S0222: 1, S6014: 1, H0441: 1, H0438: 1, H0497: 1, H0333: 1, H0069: 1, L0021: 1, H0618: 1, S0010: 1, H0421: 1, H0251: 1, H0085: 1, H0327: 1, H0178: 1, H0050: 1, H0024: 1, H0051: 1, H0375: 1, H0594: 1, H0188: 1, H0687: 1, S0022: 1, H0252: 1, H0615: 1, H0428: 1, H0622: 1, H0031: 1, H0644: 1, H0673: 1, H0674: 1,	
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579	HNGKH38	951032	589	3 - 251	1489	H0135: 1, H0163: 1, H0634: 1, H0087: 1, H0412: 1, H0056: 1, S0038: 1, H0100: 1, T0041: 1, H0429: 1, S0450: 1, S0142: 1, S0426: 1, H0529: 1, L0763: 1, L0770: 1, L0796: 1, L0761: 1, L0667: 1, L0646: 1, L0764: 1, L0771: 1, L0766: 1, L0375: 1, L0655: 1, L0657: 1, L0659: 1, L0517: 1, L0383: 1, L0382: 1, L0543: 1, L0666: 1, L0664: 1, S0374: 1, H0520: 1, H0519: 1, H0689: 1, H0682: 1, H0659: 1, H0658: 1, S0328: 1, S0027: 1, L0740: 1, L0746: 1, L0750: 1, L0759: 1, H0445: 1, L0480: 1, L0584: 1, S0242: 1, S0276: 1, H0543: 1, H0423: 1, H0422: 1, S0446: 1, L0600: 1 and H0352: 1.	AR061: 11, AR089: 5		
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									H0069: 1, H0399: 1, S0428: 1, H0698: 1 and H0521: 1.			
580	HNEHNN26	952398	590	404 - 135	1490				AR089: 1, AR061: 0 S0216: 1 and S0390: 1.			
581	HTEHP64	953791	591	304 - 2	1491	Asp-49 to Phe-54, Thr-89 to Ala-94.			AR089: 625, AR061: 610 L0666: 6, S6028: 3, L0662: 3, L0663: 3, H0038: 2, L0768: 2, S0360: 1, S0045: 1, H0574: 1, S0010: 1, H0428: 1, H0169: 1, S0036: 1, H0616: 1, L0520: 1, L0796: 1, L0657: 1, L0792: 1, L0665: 1, S0053: 1, H0547: 1, H0684: 1, S0260: 1, H0445: 1, L0599: 1 and L0593: 1.	20q13.1	256540, 600281, 600281	
582	HMLAO78	953793	592	265 - 576	1492	Ser-5 to Ser-12.			AR089: 11, AR061: 4 L0666: 6, S6028: 3, L0662: 3, L0663: 3, H0038: 2, L0768: 2, S0360: 1, S0045: 1, H0574: 1, S0010: 1, H0428: 1, H0169: 1, S0036: 1, H0616: 1, L0520: 1, L0796: 1, L0657: 1, L0792: 1,	20q13.1	256540, 600281, 600281	

583	HFPCN94	955009	593	3 - 860	1493	Pro-3 to Gly-10.	L0665: 1, S0053: 1, H0547: 1, H0684: 1, S0260: 1, H0445: 1, L0599: 1 and L0593: 1. AR089: 5, AR061: 4 L0731: 6, H0539: 5, L0065: 4, L0775: 4, L0803: 3, L0776: 3, L0663: 3, L0755: 3, S0356: 2, H0632: 2, H0545: 2, H0551: 2, L0769: 2, L0764: 2, L0662: 2, L0794: 2, L0783: 2, L0666: 2, L0750: 2, L0759: 2, H0624: 1, H0170: 1, H0583: 1, L0005: 1, H0580: 1, H0550: 1, S0222: 1, H0370: 1, H0586: 1, H0098: 1, H0318: 1, H0510: 1, H0622: 1, H0032: 1, H0169: 1, H0212: 1, S0036: 1, H0634: 1, H0022: 1, H0494: 1, S0422: 1, L0520: 1, L0796: 1, L0761: 1, L0373: 1, L0372: 1, L0806: 1, L0659: 1, L0809: 1, H0660: 1.				
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584	HSLHV08	958582	594	167 - 3	1494			AR089: 1, AR061: 0 S0428: 1 and S0028: 1.			
585	HPDVW40	961039	595	3 - 629	1495		Thr-85 to Gly-92, Pro-159 to Asn-180.	AR089: 13, AR061: 7 L0804: 5, L0758: 5, L0740: 3, L0754: 3, L0777: 3, L0604: 3, L0770: 2, L0794: 2, H0658: 2, L0752: 2, L0759: 2, L0622: 1, T0060: 1, L0021: 1, T0001: 1, L0163: 1, H0553: 1, L0769: 1, L0662: 1, L0659: 1, L0529: 1, L0789: 1, L0792: 1, S0330: 1, L0747: 1, L0749: 1 and L0485: 1.	19		
586	HEMFC70	961963	596	1 - 1164	1496		Leu-28 to Asp-35, Leu-59 to Ser-65, Glu-111 to Lys-117, Gln-131 to Ala-137, Asp-224 to Asp-233, Ala-262 to Trp-268.	AR089: 8, AR061: 5 S0046: 2, S0116: 1, S0356: 1, H0194: 1, H0051: 1, H0591: 1, H0634: 1, H0551: 1, L0564: 1, S0150: 1, H0538: 1, S0152: 1,			

							H0521: 1, S0206: 1 and H0543: 1.			
587	HLDOO20	910371	597	2 - 157	1497	Pro-21 to Arg-28.	AR061: 5, AR089: 4 L0748: 2, L0749: 2, H0510: 1 and H0144: 1.			
		963284	886	24 - 1298	1786	Glu-29 to Gly-35,				
		963655	887	1 - 1281	1787	Leu-51 to Glu-59, Gly-91 to His-98.				
588	HSLEP67	963505	598	44 - 352	1498		AR061: 0, AR089: 0 S0428: 1, S0390: 1 and S0028: 1.			
589	HSLEP94	964463	599	429 - 1355	1499		AR061: 2, AR089: 1 S0028: 5, H0624: 2, S0031: 2, H0171: 1, S0282: 1, H0250: 1, H0617: 1, H0124: 1, H0059: 1, H0144: 1, S0146: 1 and S0260: 1.			
590	HSENS89	964527	600	1 - 891	1500	Leu-1 to Phe-16.	AR089: 5, AR061: 3 H0556: 2, S0218: 1, S0132: 1, H0553: 1, H0494: 1, S0126: 1, L0602: 1, S0027: 1, L0748: 1, H0667: 1, S0276: 1 and H0423: 1.			
591	HNTAF77	966190	601	509 - 3	1501		AR089: 1, AR061: 1 L0771: 3, S0222: 2, L0731: 2, H0295: 1, H0606: 1, L0770: 1.			

592	HBIOV48	967566	602	25 - 537	1502	Ser-6 to Trp-15, Lys-18 to Gln-27, Pro-29 to Gly-35.	L0783: 1, L0791: 1, H0519: 1, L0751: 1, L0779: 1, L0755: 1 and L0759: 1. AR089: 0, AR061: 0 L0771: 4, L0803: 4, L0742: 4, L0770: 3, L0759: 3, H0194: 2, L0805: 2, L0776: 2, L0809: 2, L0789: 2, S0126: 2, S0328: 2, L0748: 2, L0779: 2, H0556: 1, S0354: 1, H0261: 1, S0010: 1, S0049: 1, H0052: 1, L0738: 1, H0105: 1, S0036: 1, H0135: 1, H0551: 1, H0538: 1, L0769: 1, L0761: 1, L0766: 1, L0649: 1, L0804: 1, L0774: 1, L0775: 1, L0659: 1, L0782: 1, L0787: 1, L0665: 1, H0593: 1, H0660: 1, H0672: 1, S0380: 1, L0741: 1, L0749: 1 and H0423: 1.			
593	HBGMN45	967744	603	2 - 562	1503		AR089: 1, AR061: 1 H0617: 2, S6028: 1 and S0028: 1			

594	HBXCE20	970889	604	2 - 403	1504		AR089: 1, AR061: 0 S0031: 4, H0624: 2, S0050: 2, H0246: 1, S0038: 1 and S0260: 1.		
595	HSLJU88	780811	605	214 - 540	1505	Ser-29 to Gly-35, Thr-82 to Val-95.	AR061: 1, AR089: 1 S0390: 2, S0278: 1 and S0144: 1.		
596	HKGDQ60	863330	606	768 - 223	1506	Arg-1 to His-9, Pro-14 to Thr-20.	AR089: 5, AR061: 2 H0261: 3, H0046: 3, L0485: 2, H0052: 1, H0538: 1 and L0745: 1.		
597	HSDKF67	933059	607	2 - 469	1507	Asn-2 to Asp-7.	AR061: 4, AR089: 1 H0271: 1 and S0260: 1.		
598	HSLFT94	603023	608	3 - 323	1508	Lys-16 to Arg-23, Gln-55 to Ile-62, Pro-99 to Asn-105.	AR089: 1, AR061: 1 S0028: 2 and S0044: 1.		
599	HTJMD06	837603	609	2 - 424	1509	Lys-35 to Lys-41, Asp-82 to Arg-88, Thr-123 to Thr-128.	AR089: 2, AR061: 1 S6028: 1, H0488: 1 and H0056: 1.		
600	HNTBH68	851274	610	1 - 540	1510	Ala-51 to Ser-57, Glu-108 to Trp-113, Phe-138 to Glu-146.	AR089: 6, AR061: 3 L0005: 1, H0144: 1, L0438: 1, H0519: 1, H0539: 1 and L0439: 1.		
601	HMEKO39	863507	611	2 - 610	1511	Pro-67 to Pro-72.	AR061: 5, AR089: 3 L0741: 5, L0751: 4, L0777: 4, S0007: 3, H0575: 3, L0747: 3, L0592: 3, S0212: 2, H0545: 2, H0266: 2, L0769: 2, L0771: 2,		

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						Ser-137 to Leu-153, Gln-155 to Gly-162, Glu-169 to Gln-178, Ser-208 to Thr-213, Arg-239 to Gly-247, Lys-253 to Leu-259, Glu-275 to Glu-281.	S0132: 1, H0266: 1, H0623: 1, H0494: 1, L0769: 1 and S0152: 1.		
604	HCEPH84	910864	614	1689 - 706	1514	Ser-65 to Gly-75, Thr-84 to Ser-89.	AR089: 1, AR061: 1 L0439: 6, L0745: 5, H0052: 4, L0438: 4, L0592: 3, L0604: 3, H0009: 2, S0001: 1, H0599: 1, H0196: 1, H0172: 1, T0010: 1, S0364: 1, S0366: 1, S0038: 1, L0789: 1, H0144: 1, S0044: 1, L0747: 1, L0759: 1 and L0605: 1.		
605	HNFD052	916260	615	2 - 358	1515		AR089: 5, AR061: 5 H0083: 17, H0556: 14, H0265: 7, L0794: 6, H0271: 5, H0543: 5, L0766: 4, L0809: 4, H0635: 2, H0150: 2, S0114: 1, H0650: 1, H0645: 1, S0222: 1, H0438: 1, H0196: 1, H0594: 1, H0416: 1, H0615: 1, H0033: 1,	2q11	129490, 600334

606	HHEJR23	919082	616	864 - 205	1516	Lys-47 to Ile-60, Ser-102 to Lys-107, Lys-152 to Ser-158, Lys-171 to Glu-176.	H0087: 1, H0488: 1, S0142: 1, L0764: 1, L0803: 1, L0655: 1, L0657: 1, L0656: 1, L0659: 1, L0783: 1, L0790: 1, L0663: 1, L0665: 1, S0216: 1, H0670: 1, H0436: 1, L0758: 1, H0595: 1, H0542: 1 and H0422: 1.	Xp11.22- p11.21	300008, 300008, 300008, 300008, 300047, 301000, 301000, 301300, 301830, 305400, 308300, 309470, 309500, 309610, 311050
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									H0648: 1, S0406: 1, L0751: 1, L0754: 1, L0779: 1, L0757: 1, L0597: 1, H0667: 1, S0242: 1, H0542: 1, H0543: 1 and L0698: 1.			
607	HMTAX31	971343	617	1091 - 522	1517	Lys-24 to Lys-36, Asp-63 to Thr-70, Arg-139 to Lys-146, Leu-156 to Ala-171.			AR050: 40, AR051: 39, AR054: 37, AR089: 5, AR061: 1 L0777: 4, S0358: 2, S0126: 2, H0522: 2, S0116: 1, H0638: 1, H0443: 1, H0014: 1, H0379: 1, S0016: 1, S0374: 1, H0518: 1, H0521: 1 and L0740: 1.			
608	HKIYI74	729217	618	3 - 347	1518	Tyr-14 to Ser-22.			AR061: 5, AR089: 3 S0045: 1, H0441: 1, H0590: 1 and L0741: 1.			
609	HSKEI21	760792	619	398 - 3	1519	Tyr-12 to Gly-19, Ser-90 to Pro-98.			AR061: 171, AR089: 34 L0751: 12, H0556: 9, L0596: 9, L0372: 5, H0265: 4, L0803: 4, S0404: 4, L0748: 4, L0758: 4, H0135: 3, L0665: 3, H0521: 3, L0742: 3, H0656: 2, H0341: 2, H0255: 2, S0418: 2, S0376: 2,			

	H0370: 2, H0575: 2, H0618: 2, H0253: 2, H0553: 2, H0038: 2, L0770: 2, L0646: 2, L0533: 2, L0375: 2, L0518: 2, L0666: 2, L0664: 2, S0238: 2, S0027: 2, L0439: 2, L0755: 2, L0759: 2, L0581: 2, H0395: 1, H0583: 1, H0484: 1, H0483: 1, H0662: 1, S0045: 1, S0046: 1, S0132: 1, H0550: 1, H0392: 1, H0586: 1, H0013: 1, H0250: 1, S0280: 1, H0599: 1, S0010: 1, H0052: 1, H0545: 1, H0046: 1, H0050: 1, H0083: 1, S6028: 1, H0687: 1, H0288: 1, S0022: 1, H0424: 1, H0111: 1, H0617: 1, H0606: 1, H0040: 1, H0616: 1, H0551: 1, H0269: 1, H0100: 1, T0042: 1, H0494: 1, H0132: 1, S0210: 1, L0762: 1, L0763: 1, L0769: 1, L0772: 1, L0374: 1,					
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610	HKA FK68	869127	620	605 - 18	1520		L0645: 1, L0662: 1, L0626: 1, L0768: 1, L0794: 1, L0766: 1, L0388: 1, L0774: 1, L0806: 1, L0776: 1, L0659: 1, H0547: 1, H0519: 1, H0435: 1, H0672: 1, H0651: 1, S0330: 1, H0539: 1, H0518: 1, S0350: 1, H0134: 1, S012: 1, S0037: 1, S0314: 1, S0028: 1, L0743: 1, L0744: 1, L0747: 1, L0750: 1, L0777: 1, L0780: 1, L0731: 1, L0587: 1, H0668: 1, S0196: 1, H0542: 1, H0422: 1, S0460: 1 and H0506: 1.		
							AR089: 3, AR061: 3 L0751: 12, H0556: 9, L0596: 8, L0372: 5, H0265: 4, L0803: 4, S0404: 4, L0748: 4, L0758: 4, H0135: 3, L0665: 3, H0521: 3, L0742: 3, H0656: 2, H0341: 2, H0255: 2, S0418: 2, S0376: 2.		

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611	HSRBB92	905110	621	2 - 2011	1521	<p>Leu-11 to Asn-16, Gly-164 to Glu-171, Leu-181 to Ser-186, Asp-193 to Ser-201, Glu-222 to Leu-229, Gln-238 to Tyr-245, Leu-256 to Asp-267, Gly-286 to Gln-301, Ser-311 to Ala-319, Glu-345 to Gly-351,</p>	<p>L0645: 1, L0662: 1, L0626: 1, L0768: 1, L0794: 1, L0766: 1, L0388: 1, L0774: 1, L0806: 1, L0776: 1, L0659: 1, H0547: 1, H0519: 1, H0435: 1, H0672: 1, H0651: 1, S0330: 1, H0539: 1, H0518: 1, S0350: 1, H0134: 1, S3012: 1, S0037: 1, S3014: 1, S0028: 1, L0743: 1, L0744: 1, L0747: 1, L0750: 1, L0777: 1, L0780: 1, L0731: 1, L0587: 1, H0668: 1, S0196: 1, H0542: 1, H0422: 1, S0460: 1 and H0506: 1.</p>	<p>AR089: 23, AR061: 4 L0779: 10, L0747: 8, L0758: 7, L0766: 4, L0776: 4, L0748: 4, L0740: 4, S0360: 3, H0616: 3, L0754: 3, L0731: 3, L0759: 3, L0599: 3, L0362: 3, H0543: 3, H0341: 2, H0013: 2, H0024: 2,</p>	<p>120260, 138140, 178300, 246450</p>
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613	HWLWQ87	932577	623	76 - 519	1523	Glu-44 to Gly-50, Pro-104 to Gly-111, Gly-127 to Leu-132, Asn-146 to Asp-151, Asn-165 to Glu-170, Ser-194 to Asp-202. Ile-111 to Glu-19.	S0358: 1, H0370: 1, H0253: 1, H0040: 1, H0547: 1, L0601: 1 and S0196: 1. AR089: 23, AR061: 12 L0731: 6, L0766: 5, L0759: 5, L0471: 2, H0038: 2, L0748: 2, L0740: 2, L0758: 2, L0590: 2, S0360: 1, H0596: 1, H0046: 1, L0483: 1, H0644: 1, H0616: 1, H0509: 1, H0647: 1, S0210: 1, L0648: 1, L0363: 1, L0774: 1, L0775: 1, L0657: 1, L0526: 1, L0666: 1, L0664: 1, S0126: 1, H0672: 1, L0744: 1, L0593: 1, L0595: 1, H0665: 1 and S0194: 1.		
614	H6EEP53	942872	624	3 - 1595	1524		AR061: 1, AR089: 1 L0748: 8, L0769: 7, L0758: 7, L0749: 5, H0135: 4, S0418: 3, S0358: 3, H0618: 3, H0424: 3 H0529: 3		

			L0439: 3, L0747: 3, L0779: 3, L0777: 3, H0265: 2, S0356: 2, S0360: 2, S0278: 2, H0257: 2, H0559: 2, H0156: 2, H0596: 2, H0232: 2, H0544: 2, H0510: 2, H0031: 2, H0087: 2, T0041: 2, H0494: 2, S0344: 2, L0764: 2, L0766: 2, L0664: 2, L0438: 2, H0547: 2, H0539: 2, H0522: 2, H0555: 2, L0751: 2, L0757: 2, L0587: 2, L0605: 2, L0411: 1, H0686: 1, H0295: 1, H0341: 1, S0001: 1, H0483: 1, H0255: 1, H0664: 1, H0306: 1, H0458: 1, S0376: 1, H0580: 1, L0717: 1, H0550: 1, S0222: 1, H0592: 1, H0497: 1, L0622: 1, H0013: 1, H0253: 1, H0318: 1, H0052: 1, H0546: 1, H0046: 1, H0012: 1, H0373: 1, H0083: 1, H0399: 1, H0288: 1, H0290: 1,						
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615	HE2KZ56	968439	625	82 - 342	1525	AR089: 2 AR061: 1	H0252: 1, T0006: 1, H0213: 1, H0553: 1, H0644: 1, H0673: 1, H0068: 1, H0038: 1, H0040: 1, H0551: 1, H0413: 1, H0100: 1, H0131: 1, S0150: 1, S0144: 1, S0422: 1, L0369: 1, L0763: 1, L0646: 1, L0643: 1, L0645: 1, L0773: 1, L0662: 1, L0768: 1, L0364: 1, L0650: 1, L0774: 1, L0775: 1, L0378: 1, L0776: 1, L0657: 1, L0659: 1, L0783: 1, L0666: 1, L0665: 1, S0428: 1, H0144: 1, H0520: 1, H0519: 1, H0435: 1, H0658: 1, H0666: 1, H0518: 1, H0521: 1, H0696: 1, L0609: 1, S3014: 1, S0027: 1, L0741: 1, L0744: 1, L0754: 1, L0752: 1, L0731: 1, L0759: 1, L0596: 1, H0665: 1, H0423: 1 and S0446: 1.		
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616	HFHXHD52	490721	626	191 - 3	1526	Asn-44 to Ala-51.	H0624: 2 and S0031: 1. S0001: 1, S0045: 1 and S0216: 1.		
		883683	888	1 - 279	1788	Phe-2 to Ser-8, Glu-58 to Gln-63, Asn-74 to Leu-81.			
617	HPMAM67	915879	627	2 - 64	1527		L0777: 20, L0439: 11, L0747: 10, S0360: 6, L0766: 6, L0758: 6, L0717: 5, H0521: 5, H0038: 3, S0330: 3, L0752: 3, L0755: 3, L0599: 3, S0358: 2, H0581: 2, S0003: 2, S0214: 2, H0068: 2, L0764: 2, L0662: 2, L0655: 2, L0666: 2, L0665: 2, H0648: 2, L0740: 2, L0751: 2, L0749: 2, L0750: 2, L0731: 2, L0757: 2, S0031: 2, L0596: 2, L0581: 2, L0362: 2, S0192: 2, H0542: 2, S0040: 1, H0650: 1, H0657: 1, S0282: 1, H0580: 1, H0393: 1, H0586: 1, H0574: 1, H0486: 1, L0586: 1, H0013: 1, L0021: 1,		

618	HBXFI75	959570	889	241 - 26	1789	Glu-1 to Glu-7, Ile-14 to Thr-19.	H0036: 1, H0318: 1, L0563: 1, H0545: 1, S0051: 1, T0010: 1, H0375: 1, H0188: 1, H0119: 1, H0031: 1, H0591: 1, H0040: 1, H0616: 1, T0067: 1, H0488: 1, H0412: 1, H0100: 1, H0652: 1, S0344: 1, S0002: 1, L0369: 1, L0763: 1, L0769: 1, L0638: 1, L0761: 1, L0772: 1, L0646: 1, L0768: 1, L0389: 1, L0774: 1, L0775: 1, L0375: 1, L0776: 1, L0659: 1, L0382: 1, L0809: 1, H0520: 1, H0547: 1, H0435: 1, H0658: 1, H0670: 1, H0672: 1, S0328: 1, H0555: 1, H0478: 1, L0756: 1, L0779: 1, H0444: 1, H0445: 1, L0366: 1, S0011: 1 and S0026: 1.	
		566766	628	489 - 1295	1528	Cys-32 to Cys-39, Glu-47 to Pro-52.	AR061: 0, AR089: 0 H0305: 3, L0105: 3.	

619	HELM94	913938	629	1 - 1437	1529	<p>Lys-57 to Pro-62, Ser-108 to Ala-114, Asp-133 to Arg-140, Arg-173 to Asn-183.</p> <p>Cys-32 to Cys-39, Glu-47 to Pro-52, Lys-57 to Pro-62, Ser-108 to Ala-114, Asp-133 to Arg-140, Arg-173 to Asn-183.</p> <p>Asp-72 to Glu-78, Ser-103 to Glu-110, Lys-112 to His-117.</p> <p>Lys-42 to Pro-47, Ser-93 to Ala-99, Asp-118 to Arg-125, Arg-158 to Asn-168, Ala-251 to Val-263, His-287 to Tyr-292, Glu-302 to Gln-307.</p> <p>Gly-1 to Ser-8, Arg-10 to Ser-15, Leu-17 to Gly-22, Lys-115 to Ala-130, Tyr-149 to Gly-156, Asn-181 to Glu-190, Glu-252 to Glu-257, Ser-339 to Asp-347, Leu-356 to Leu-361.</p>	<p>489 - 1295</p> <p>30 - 647</p> <p>748 - 1923</p>	<p>1790</p> <p>1791</p> <p>1792</p>	<p>L0608: 3, H0624: 1, H0589: 1, H0438: 1, H0250: 1, S0050: 1, H0135: 1, S0144: 1, H0689: 1 and S0028: 1.</p> <p>AR089: 9, AR061: 5, H0584: 5, H0599: 5, H0556: 4, H0124: 4, H0559: 3, H0622: 3, H0341: 2, H0125: 2, S0045: 2, H0620: 2, H0024: 2, T0042: 2, L0665: 2, H0144: 2, H0265: 1, S6024: 1.</p>	16p11.2	147781, 172471, 182381
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						Ser-387 to Lys-395, Thr-470 to Ile-476.	H0583: 1, H0208: 1, S0046: 1, H0393: 1, S0278: 1, H0549: 1, H0550: 1, H0438: 1, H0586: 1, H0486: 1, H0250: 1, S0280: 1, H0618: 1, H0253: 1, H0009: 1, H0687: 1, H0284: 1, H0424: 1, H0031: 1, S0366: 1, H0116: 1, H0056: 1, S0038: 1, H0494: 1, H0132: 1, H0131: 1, H0130: 1, L0662: 1, L0803: 1, S0428: 1, S0216: 1, S0126: 1, H0518: 1, S0152: 1, S0118: 1, S014: 1, L0759: 1 and S0011: 1.		
620	HLJDQ52	923110	630	3 - 824	1530	Gly-26 to Val-70, Ser-199 to Arg-204.	AR089: 15, AR061: 1 T0109: 1, H0013: 1, H0375: 1, H0509: 1, H0519: 1, H0690: 1, S0152: 1 and L0485: 1.		
621	HAAW40	1219455	631	68 - 2323	1531	Pro-7 to Arg-12, Leu-32 to His-52, Tyr-54 to Asp-69, Pro-74 to Gly-92, Glu-99 to Arg-125, Asp-130 to Glu-142,	AR089: 4, AR061: 1 L0803: 5, L0731: 4, L0662: 3, L0665: 3, S0276: 3, H0486: 2, H0575: 2, H0318: 2, L0794: 2, L0805: 2,		

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623	HBUC02	908326	894	3 - 809	1794	Asn-23 to Trp-32, Ile-49 to Asp-56, Gln-85 to Pro-91.	AR089: 13, AR061: 8 S0152: 4, H0556: 3, H0265: 2, S3014: 2, H0543: 2, H0423: 2, H0161: 1, H0650: 1, H0402: 1, S0045: 1, S0046: 1, H0393: 1, H0599: 1, H0575: 1, H0618: 1, H0253: 1, S0182: 1, H0083: 1, H0594: 1, H0247: 1, H0124: 1, H0652: 1, S0144: 1, H0519: 1, H0651: 1, S0027: 1 and H0445: 1.
		1220017	633	3 - 668	1533	Ala-8 to Thr-23, Pro-35 to Met-41, Asn-60 to Thr-65, Asn-89 to Glu-94, Pro-161 to Leu-167, Asp-184 to Trp-189, Phe-192 to Leu-206, Arg-215 to Leu-221.	
		933546	895	3 - 818	1795	Ala-8 to Thr-23, Pro-35 to Met-41, Asn-60 to Thr-65, Asn-89 to Glu-94, Pro-161 to Leu-167, Asp-184 to Trp-189, Phe-192 to Pro-201, Pro-226 to Lys-231, Ala-237 to Pro-264.	
624	HCWEQ14	1117318	634	319 - 77	1534		AR089: 39, AR061: 8 H0305: 3
		908245	896	1 - 177	1796	Leu-43 to Tyr-48.	

625	HDPWH41	1228148	635	1 - 642	1535	AR089: 6, AR061: 2 S0252: 5, S0268: 5, S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0657: 1, S0212: 1, H0661: 1, H0580: 1, L0717: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0412: 1, L0637: 1, L0766: 1, L0791: 1, S0216: 1, H0670: 1, S0380: 1, L0755: 1, H0445: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1 and H0543: 1.		
626	HDQEH61	1213567	636	46 - 867	1536	AR089: 63, AR061: 13 H0616: 3, H0521: 3, H0046: 2, H0038: 2, S0045: 1, H0550: 1, H0013: 1, S0386: 1, H0494: 1, S0150: 1, H0520: 1, H0436: 1 and L0595: 1.		
		772569	897	1 - 369	1797	Arg-68 to Ser-76.		
		908303	898	2 - 766	1798	Gln-49 to Thr-58, Pro-175 to Lys-184.		

627	HDTDD72	587710	637	162 - 371	1537		AR089: 159, AR061: 142 H0486: 1	17p13.3	113721, 247200, 600059, 601545
628	HFRBN02	1152485	638	2 - 967	1538	Gly-114 to Gly-120, Pro-140 to Tyr-145, Asn-180 to Gly-185, Arg-274 to Ala-280, Gly-310 to Gly-317.	AR089: 3, AR061: 1 S0045: 1, S0050: 1, H0020: 1 and S0032: 1.		
629	HKAHH72	973667	899	2 - 409	1799	Gly-114 to Gly-120.			
		1107045	639	1 - 642	1539	Pro-9 to Ala-19, Ser-39 to Gly-46, Thr-54 to Gly-62, Ile-77 to Arg-84, Thr-122 to Met-132, Gln-134 to Gln-147.	AR089: 2, AR061: 2 L0766: 2, L0665: 2, H0395: 1, S0212: 1, S0360: 1, H0551: 1, H0494: 1, L0639: 1, L0521: 1, L0804: 1, H0682: 1 and L0749: 1.		
		761293	900	1 - 690	1800	Pro-9 to Ala-19, Ser-39 to Gly-46, Thr-54 to Gly-62, Ile-77 to Arg-84, Thr-122 to Met-132, Gln-134 to Gln-147.			
630	HMAAD90	1152487	640	334 - 2	1540	Ser-15 to Gln-23, Gly-79 to Asp-92, Gly-105 to Cys-111.	AR089: 2, AR061: 1 L0769: 7, L0783: 6, L0775: 5, L0748: 4, L0758: 4, L0622: 3, H0599: 3, H0373: 3, L0772: 3, L0777: 3, L0757: 3, S0045: 2,		

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631	HMABQ71	1105540	641	3 - 374	1541	His-173 to Asp-178, Arg-196 to Ser-202, Arg-214 to Val-220, Ser-243 to Leu-253, Arg-275 to Ile-283, Lys-367 to Phe-374, Gln-384 to Gly-389, Glu-430 to Lys-440.	AR089: 1, AR061: 0 S0144: 1 and H0521: 1.	
632	HPJEV95	729831	902	189 - 497	1802		AR061: 4, AR089: 1 S0152: 1 and L0601: 1.	
633	HSKYR59	929723	903	82 - 408	1803	His-91 to Gly-103, Gly-112 to Gly-117, Glu-129 to Glu-136, Gly-146 to Gly-151, Arg-168 to Glu-184, Arg-203 to Arg-210.	AR061: 16, AR089: 6 H0617: 10, S0358: 5, L0622: 4, H0620: 4, H0658: 4, L0623: 3, H0424: 3, H0549: 2, H0550: 2, H0586: 2, H0486: 2, H0546: 2, L0769: 2, L0773: 2, S0374: 2, S0206: 2, L0743: 2, L0750: 2, L0779: 2, L0731: 2, L0601: 2, H0624: 1, H0170: 1, H0171: 1, H0686: 1, H0295: 1, H0657: 1, H0484: 1, H0255: 1, S0420: 1,	

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	H0617: 10, S0358: 5, L0622: 4, H0620: 4, H0658: 4, L0623: 3, H0424: 3, H0549: 2, H0550: 2, H0586: 2, H0486: 2, H0546: 2, L0769: 2, L0773: 2, S0374: 2, S0206: 2, L0743: 2, L0750: 2, L0779: 2, L0731: 2, L0601: 2, H0624: 1, H0170: 1, H0171: 1, H0686: 1, H0295: 1, H0657: 1, H0484: 1, H0255: 1, S0420: 1, S0376: 1, S0360: 1, H0370: 1, H0455: 1, H0587: 1, T0060: 1, T0114: 1, H0599: 1, H0122: 1, H0327: 1, H0544: 1, H0545: 1, H0188: 1, H0688: 1, T0006: 1, H0213: 1, H0606: 1, H0673: 1, S0364: 1, S0366: 1, H0634: 1, H0087: 1, H0413: 1, H0334: 1, S0144: 1, L0598: 1, L0763: 1, L0796: 1, L0639: 1, L0761: 1, L0772: 1, L0373: 1,	
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635	HSXCW82	933749	905	11 - 604	1805	Ala-2 to Gly-15, Glu-120 to Ser-125.	L0764: 1, L0774: 1, L0775: 1, L0783: 1, L0809: 1, L0666: 1, L0663: 1, H0651: 1, S0378: 1, H0521: 1, S0392: 1, H0478: 1, L0751: 1, L0747: 1, L0752: 1, L0755: 1, L0757: 1, H0445: 1, L0608: 1, L0361: 1, L0366: 1, H0542: 1 and H0543: 1.		
		1164013	645	123 - 1442	1545	Leu-14 to Ile-19, Pro-69 to Pro-76, Glu-86 to Thr-91, Val-121 to Thr-127, Phe-183 to Gln-188, Gly-282 to Lys-291, Arg-337 to Asn-346.	AR061: 6, AR089: 5, H0556: 8, H0617: 6, L0659: 6, L0666: 6, L0596: 6, H0441: 5, L0665: 5, S0222: 4, T0010: 4, S0038: 4, H0657: 3, H0559: 3, H0013: 3, H0494: 3, L0804: 3, L0809: 3, H0547: 3, S0152: 3, H0521: 3, H0265: 2, H0656: 2, L0717: 2, S0278: 2, H0250: 2, H0575: 2, S0049: 2, H0620: 2, H0288: 2, H0213: 2, S0036: 2.		

	H0634: 2, H0623: 2, L0764: 2, L0766: 2, L0775: 2, L0438: 2, H0682: 2, S0028: 2, L0779: 2, L0758: 2, L0595: 2, H0422: 2, H0224: 1, S0430: 1, L0785: 1, H0341: 1, S0212: 1, H0663: 1, S0420: 1, H0637: 1, H0580: 1, H0437: 1, H0282: 1, H0249: 1, T0109: 1, H0244: 1, H0069: 1, S0346: 1, H0318: 1, H0052: 1, H0194: 1, N0006: 1, L0471: 1, H0024: 1, H0057: 1, L0163: 1, H0107: 1, H0083: 1, H0594: 1, S0336: 1, H0070: 1, T0006: 1, H0644: 1, H0181: 1, H0135: 1, H0090: 1, H0040: 1, H0087: 1, H0059: 1, H0100: 1, L0351: 1, T0041: 1, H0429: 1, H0647: 1, S0210: 1, S0002: 1, H0529: 1, L0369: 1, L0769: 1, L0761: 1, L0372: 1, L0800: 1,	
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636	HSYDB42	739372	906	115 - 387	1806	Leu-14 to Ile-19.	L0794: 1, L0803: 1, L0806: 1, L0509: 1, L0657: 1, L0383: 1, L0787: 1, L0663: 1, S0374: 1, H0593: 1, H0658: 1, H0522: 1, H0134: 1, H0555: 1, L0612: 1, S3012: 1, S0037: 1, S3014: 1, S0206: 1, L0439: 1, L0749: 1, L0752: 1, S0031: 1, L0592: 1, L0608: 1, L0366: 1, H0667: 1, S0276: 1, H0542: 1 and H0423: 1.	22q13.1-q13.2	103050, 103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040
636	HSYDB42	933545	646	2 - 631	1546	Arg-1 to Thr-11, Pro-23 to Met-29, Asn-48 to Thr-53, Asn-77 to Glu-82, Pro-149 to Leu-155, Asp-172 to Trp-177, Phe-180 to Leu-194, Arg-203 to Leu-209.	AR061: 2, AR089: 1 H0305: 5, L0766: 3, L0748: 3, H0265: 2, H0556: 2, H0551: 2, H0494: 2, L0770: 2, L0758: 2, L0599: 2, L0361: 2, H0650: 1, H0657: 1, H0381: 1, H0419: 1, H0427: 1, H0618: 1, H0421: 1, H0530: 1, H0546: 1, H0413: 1, H0625: 1, L0369: 1, L0644: 1, L0521: 1, L0375: 1,		

637	HTXKJ79	1193059	647	2 - 421	1547	Pro-3 to Leu-9, Glu-12 to Val-22, Gln-27 to Glu-33, Pro-68 to Glu-75.	L0783: 1, L0809: 1, L0789: 1, H0144: 1, S0374: 1, L0565: 1, H0658: 1, S0330: 1, H0539: 1, L0777: 1, L0731: 1, H0542: 1 and H0506: 1.	L0783: 1, L0809: 1, L0789: 1, H0144: 1, S0374: 1, L0565: 1, H0658: 1, S0330: 1, H0539: 1, L0777: 1, L0731: 1, H0542: 1 and H0506: 1.	
							AR089: 3, AR061: 3 L0748: 9, S0356: 8, S0358: 8, L0471: 5, H0144: 5, L0740: 5, H0543: 5, H0574: 4, H0556: 3, S0354: 3, S0360: 3, S0049: 3, H0083: 3, T0042: 3, H0494: 3, S0374: 3, H0134: 3, H0436: 3, H0624: 2, H0663: 2, S0007: 2, S0132: 2, H0486: 2, H0013: 2, H0036: 2, H0251: 2, H0009: 2, S0036: 2, H0412: 2, H0561: 2, S0142: 2, H0522: 2, L0750: 2, L0588: 2, H0159: 1, H0583: 1, H0656: 1, H0341: 1, S0212: 1, H0240: 1, H0125: 1, S0418: 1, S0420: 1, S0410: 1.	AR089: 3, AR061: 3 L0748: 9, S0356: 8, S0358: 8, L0471: 5, H0144: 5, L0740: 5, H0543: 5, H0574: 4, H0556: 3, S0354: 3, S0360: 3, S0049: 3, H0083: 3, T0042: 3, H0494: 3, S0374: 3, H0134: 3, H0436: 3, H0624: 2, H0663: 2, S0007: 2, S0132: 2, H0486: 2, H0013: 2, H0036: 2, H0251: 2, H0009: 2, S0036: 2, H0412: 2, H0561: 2, S0142: 2, H0522: 2, L0750: 2, L0588: 2, H0159: 1, H0583: 1, H0656: 1, H0341: 1, S0212: 1, H0240: 1, H0125: 1, S0418: 1, S0420: 1, S0410: 1.	

							S0045: 1, H0411: 1, H0369: 1, H0586: 1, H0497: 1, H0643: 1, H0331: 1, S0010: 1, H0052: 1, H0327: 1, H0544: 1, H0545: 1, H0011: 1, H0012: 1, H0014: 1, H0015: 1, H0239: 1, H0266: 1, H0688: 1, H0124: 1, H0135: 1, H0040: 1, H0413: 1, H0059: 1, H0280: 1, S0344: 1, H0529: 1, H0691: 1, H0547: 1, H0519: 1, H0682: 1, H0660: 1, S0328: 1, H0518: 1, H0521: 1, S0037: 1, S3014: 1, S0028: 1, L0742: 1, L0752: 1, L0755: 1, S0026: 1, H0136: 1 and H0293: 1.	
							AR089: 2, AR061: 2 S0252: 5, S0268: 5, S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0657: 1,	

639	HUSZS75	1193982	649	1 - 519	1549	Arg-54 to Pro-67, Arg-82 to Ala-90, Gln-105 to Asp-115.	Arg-1 to Asp-13, Arg-81 to Ser-89, Gly-128 to Gly-143.	772568	908	2 - 517	1808	S0212: 1, H0661: 1, H0580: 1, L0717: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0412: 1, L0637: 1, L0766: 1, L0791: 1, S0216: 1, H0670: 1, S0380: 1, L0755: 1, H0445: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1 and H0543: 1.		
												AR089: 1, AR061: 1, L0769: 10, L0754: 10, L0766: 5, L0803: 4, L0756: 4, L0779: 4, L0780: 4, L0748: 3, L0753: 3, H0620: 2, H0264: 2, L0770: 2, L0806: 2, L0741: 2, L0747: 2, L0604: 2, H0265: 1, H0556: 1, H0657: 1, H0656: 1, H0341: 1, H0392: 1, H0331: 1, H0559: 1, H0427: 1, L0021: 1, H0173: 1, H0052: 1,		

640	HWBDR25	908443 1174365	909 650	64 - 918 3 - 1259	1809 1550	Arg-7 to Thr-13. Pro-1 to Glu-13, Gln-29 to Asn-35, Tyr-38 to Asn-43, Ala-102 to Ser-108, Arg-124 to Ile-134, Asp-172 to Asp-180, Lys-247 to Asn-252, Gly-336 to Trp-342. Lys-37 to Asn-42, Gly-126 to Trp-132.	AR089: 5, AR061: 1 H0551: 2, S0420: 1, H0580: 1, H0586: 1, S0002: 1, H0435: 1 and H0521: 1.		
641	HBGSS51	954855	651	341 - 3	1551		AR061: 5, AR089: 4 L0771: 12, H0040: 2, H0539: 2, H0306: 1, H0617: 1 and H0135: 1.		

[42] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

[43] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.

[44] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.

[45] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A.

It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[46] Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

[47] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is

assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[48] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[49] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIM™ (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

Clone ID NO:Z	SEQ ID NO:X	CONTIG ID:	BAC ID: A	SEQ ID NO:B	EXON From-To
HADTU18	26	666268	AC067849	1811	1-1270
HADTU18	26	666268	AC067849	1812	1-408
HYAAH23	42	1032585	AL158156	1813	1-134 381-1154 1539-2051 2660-4011 4082-4116 4578-5063 5736-6373 6388-6981 7052-7364 7527-7659 7698-7943 9535-9659 9671-10133 11759-12221
HYAAH23	42	1032585	AL158155	1814	1-171 2177-2317 2558-3332 3786-4298 4772-6123 6194-6228 6690-7175 7848-8485 8500-9065 9164-9476 9639-9771 9810-10055 11647-11771 11783-12245 13870-14332
HYAAH23	42	1032585	AL158156	1815	1-4481
HYAAH23	42	1032585	AL158155	1816	1-4477
HAJAV28	45	948630	AL121579	1817	1-175 1520-1889 2329-2473 2730-2805 3231-3444 4096-4273 7815-7900 8874-9058
HCE1S21	49	671209	AC007666	1818	1-122 274-371

					3724-3890 4511-4668 5669-6372 6679-7654
HCE1S21	49	671209	AC000052	1819	1-122 274-371 1127-1238 3724-3890 4511-4668 5669-6372 6679-7654
HCE1S21	49	671209	AC004019	1820	1-122 274-371 1127-1238 3724-3890 4511-4668 5669-6372 6679-7654
HCE1S21	49	671209	AC007666	1821	1-269 324-413
HCE1S21	49	671209	AC007666	1822	1-591 2367-2471 4522-4940 4990-5100 6036-6133 6225-6754 7871-7959 8764-9481
HCE1S21	49	671209	AC000052	1823	1-269 324-413
HCE1S21	49	671209	AC000052	1824	1-591 2366-2473
HCE1S21	49	671209	AC004019	1825	1-269 324-413
HCE1S21	49	671209	AC004019	1826	1-462
HCE3J64	50	951228	AC061705	1827	1-77 614-729 917-1028 1154-1218 1398-1591 1704-1802 2419-3315
HCFLI54	52	921382	AC023278	1828	1-1977 2006-3504 3802-4090 4113-6041 6143-6242 6252-6919

					6933-7614 7682-8351
HCFLI54	52	921382	AC005562	1829	1-3490 3783-4087 4094-6238 6249-6901 6930-7364 7701-8350
HCFLI54	52	921382	AC023278	1830	1-574 774-1443
HCFLI54	52	921382	AC023278	1831	1-616
HCFLI54	52	921382	AC005562	1832	1-667
HCWDL45	55	889416	AC023100	1833	1-1181
HCWDL45	55	889416	Z98747	1834	1-1181
HDPGQ74	59	691163	AC073462	1835	1-173 1923-2056 2270-2362 4504-5101 5444-5630 6218-6268 8466-8542 8816-8888 10396-10437
HDPGS68	60	752975	AC034180	1836	1-950
HE2FR50	64	508498	AC010408	1837	1-574 1043-1729 1759-1995 2866-3391 3406-3626 3954-4396 4444-4667 5413-5515 8692-8774 8878-9828 13011-13373 14082-14365 15285-16319
HEBGK01	67	963673	Z97653	1838	1-627 815-1256 2165-2714
HEBGK01	67	963673	Z97653	1839	1-146
HEBGK01	67	963673	Z97653	1840	1-487
HEFMB30	68	691516	AC016659	1841	1-862
HEFMB30	68	691516	AC012481	1842	1-862
HEFMB30	68	691516	AC016659	1843	1-447
HEFMB30	68	691516	AC012481	1844	1-447
HEOPE58	69	851009	AL078634	1845	1-40 1089-1226

					3206-3637 4312-4463 7455-8330 8603-8815 9078-9190 9522-9767 10946-12260 13754-14357 15092-15830 18660-18822 21128-21635 21685-21721
HEOPE58	69	851009	AL078634	1846	1-235 3051-3154 3199-3734
HEOPE58	69	851009	AL078634	1847	1-444
HLHDD45	75	942901	AC024148	1848	1-116 629-787 1238-1305 1825-1969 2522-2966 2984-6238
HLHDD45	75	942901	AC069253	1849	1-116 629-787 1238-1305 1824-1968 2521-2965 2983-5879
HLHDD45	75	942901	AC044892	1850	1-116 629-787 1238-1305 1824-1968 2521-2965 2983-6236
HLHDD45	75	942901	AC044892	1851	1-105
HLHDD45	75	942901	AC069253	1852	1-105
HNHEQ86	79	785580	AC024653	1853	1-731
HSICX21	88	531267	AC016333	1854	1-552
HSICX21	88	531267	AC024101	1855	1-551
HSICX21	88	531267	AC016333	1856	1-448
HSICX21	88	531267	AC024101	1857	1-447
HSODC08	91	966264	AC005332	1858	1-1096 1112-1196 2142-2580 2893-3071 3148-3485 4737-5087 6182-6336

					6503-6667 7642-8422 8767-9265
HSODC08	91	966264	AC005332	1859	1-205 221-693
HSODC08	91	966264	AC005332	1860	1-181
HSQCM85	93	963554	AL021918	1861	1-629
HTOIA82	94	844319	AC012446	1862	1-410
HTOIA82	94	844319	AC012446	1863	1-329
HUUDH57	95	931155	AC009073	1864	1-118 2843-2982 5373-5675 6891-7201 8485-8641 9497-9900 10048-10506 10621-11749 12563-12695 12919-13053 14526-14766 16311-16378 17695-17869 18462-18541 19565-19750 21028-21485 25002-26608 26801-28071 28114-28369 28825-28998 29505-29648 31878-31961 32637-32809 32835-32936 33645-35911
HWAFFW39	97	947915	AC008508	1865	1-124 2706-3000 3745-3882 5914-6036 6110-6413 6491-6844 6912-7681 8888-9020 10437-10570 10686-11022
HWAFFW39	97	947915	AC008955	1866	1-544 2059-2219 2947-3088 5596-5891

					6635-6773 8782-8904 8978-9281 9359-9712 9778-10496
HWAFW39	97	947915	AC008963	1867	1-124 2645-2940 3685-3822 5831-5953 6027-6330 6408-6761 6828-7597 8806-8938 10353-10487 10603-10939 12315-12471 13563-13693 14450-14528 15001-16291
HWAFW39	97	947915	AC009073	1868	1-240 2827-3055 4160-4703 6218-6382 7102-7248 9770-10061 10805-10943 12952-13074 13148-13451 13529-13882 13951-14720 15927-16059 17474-17607 17723-18059 19435-19592 20686-20816 21573-21651 22124-23668 24035-24199 24212-24595 24879-25065 25816-26017 26260-26422 26424-26555 26824-27350 27380-27598 27609-27697 29321-29822 30645-30922

					31155-31244 31552-35653 35933-36067 36391-38070 38077-38991 39063-39584 40088-40196 40614-40660 41408-41837 41924-42048 42066-42712 42745-42876 43068-43760 43825-44062 44913-46162 46311-47285 47523-47779 50015-50221 50441-50512 50601-50653 50832-51143 52660-53226 53353-53439 53447-53826 53936-54038 57264-57491 59462-59560
HWAFW39	97	947915	AC009073	1869	1-452
HWAFW39	97	947915	AC008955	1870	1-229
HWAFW39	97	947915	AC008963	1871	1-146
HBGDA14	114	866258	AC074220	1872	1-919
HBGDA14	114	866258	AC024580	1873	1-682
HDPND85	119	852628	AC003042	1874	1-261 1877-2339 3059-3286 3970-4326 4931-5114 6268-6359 7022-7866 7877-8140 8262-8911
HDPND85	119	852628	AC003042	1875	1-754 955-1048 6079-6214 6309-6423 6705-7373
HE9RE21	122	888243	AC040908	1876	1-203
HKABI68	125	856590	AC007606	1877	1-650

					709-802 3445-3584 3925-4225 4428-4595 5220-5285 5346-5673 5789-5962 7106-7206 8427-8807 9869-10247 10688-11328 11382-12036 12610-13224
HKABI68	125	856590	AC007606	1878	1-1215 1651-1783 1974-2304 2681-2756
HWHPO29	134	857383	AL049779	1879	1-210 1909-2318 2599-2753 3548-3655 4479-4690 6391-6879 7696-8065 10475-10649 11240-11950
HNTMD81	167	929511	AL138795	1880	1-327 2886-2923 3052-3182 3604-3784 4304-4446 4671-4764 4948-5014 5186-5345 5443-5566 5923-6025 6558-8807 9222-9363 9502-9626 9862-9937 10087-10280 10803-11470
HNTMD81	167	929511	AL365403	1881	1-133 358-451 635-701 873-1032 1130-1253 1610-1712

					2245-2912
HNTMD81	167	929511	AL365403	1882	1-131
HNTMD81	167	929511	AL138795	1883	1-634
HSKCI43	169	506599	AC068494	1884	1-826
HAMFW05	230	957586	AC005594	1885	1-103 2099-2278 2831-3511 4124-4482 6695-6777 7930-8084 8758-8898 9553-9738 10471-10829 11883-12031 12754-12992 13983-14296 14330-14468 14814-14959 15524-15766 17708-17819 18969-19670 20698-22428
HAMFW05	230	957586	AC005594	1886	1-232
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HBGSS51	651	954855	AC012615	2317	1-451
HBGSS51	651	954855	AC012615	2318	1-2083 2996-3117 3196-3330 3338-3638 3847-4160 4362-4596 5559-6225 6740-7087 7196-7297 7410-7746 7903-8059 8362-8495 8982-9518 10231-10522 11163-11210

[50] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

Clone ID NO:Z	Contig ID:	SEQ ID NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
HHMMC14	1152250	11	blastx.2	GLYOXYLATE REDUCTASE (EC 1.1.1.79).	sp Q9UBQ7 Q9UBQ 7	96%	105	1088
HHMMC14	969371	652	HMMER 1.8	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	217.83	336	965
HSLEQ79	1184946	12	blastx.14	(AF146018) hydroxypyruvate reductase [Homo sapiens]	gi 5639830 gb AAD4 5886.1 AF146018_1	96%	87	1070
HSLEQ79	1184946	12	blastx.2	D-lactate dehydrogenase (EC 1.1.1.28) - Escherichia coli	pir G64888 G64888	93%	674	156
HSLEQ79	752382	653	HMMER 2.1.1	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	222	19	453
HUCME08	1082023	13	blastx.2	GLYOXYLATE REDUCTASE (EC 1.1.1.79).	sp Q9UBQ7 Q9UBQ 7	88% 100%	110 54	625 107
HUCME08	868780	654	HMMER 2.1.1	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	93.4	275	556
HNGOW33	1152254	14	blastx.2	8-amino-7-oxononanoate synthase (EC 2.3.1.47) - Escherichia coli	pir D32025 SYBCKP	91% 70%	547 336	1158 497

HNGOW33	957351	655	HMMER 2.1.1	PFAM: Aminotransferases class-II (AE000195) orf, hypothetical protein [Escherichia coli]	PF00222	441.9	409	1251
			blastx.14		gi 1787167 gb AAC7 4022.1	99%	2714	3712
HT4GD03	1103896	15	blastx.2	2-AMINO-3- KETOBUTYRATE COENZYME A LIGASE, MITOCHONDRIAL 1	sp O75600 KBL_HU MAN	93% 100%	153 89	968 166
HT4GD03	923731	656	HMMER 1.8	PFAM: Aminotransferases class-II	PF00222	78.93	575	877
			blastx.14	d 466N1.2 (2-amino-3- ketobutyrate-CoA ligase mRNA, 1	gi 4808241 emb CAB 42830.1	100% 87% 100%	584 153 140	967 569 166
HAQBZ89	949061	16	HMMER 1.8	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	62.49	68	325
			blastx.2	CG8745 PROTEIN.	sp Q9VU95 Q9VU95	52%	8	316
HCCCC81	949062	17	HMMER 1.8	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	178.37	187	816
			blastx.2	hypothetical protein T01B11.2 - Caenorhabditis elegans	pir T25848 T25848	46%	190	879
HE8PW83	927532	18	HMMER 1.8	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	139.27	4	465
			blastx.2	ALANINE-- GLYOXYLATE AMINOTRANSFERASE	sp Q64565 AGT2_R AT	83%	4	546

HE9QQ22	949080	19	HMMER 2.1.1	2 PRECURSOR (EC 1.1 PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	105.1	285	545
			blastx.2	ALANINE-- GLYOXYLATE AMINOTRANSFERASE	sp Q64565 AGT2_R AT	51% 43% 49%	3 545 682	1070 1003 999
HFPFB39	946170	20	HMMER 1.8	2 PRECURSOR (EC 1.1 PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	235.05	1613	714
			blastx.2	hypothetical protein T01B11.2 - Caenorhabditis elegans	pir T25848 T25848	49%	1613	651
HSDJI44	1151680	21	blastx.2	adenosylmethionine--8- amino-7-oxononanoate transaminase (EC 2.6.1.62) - Escherichia coli	pir F64813 XNECDP	96%	857	2143
HSDJI44	974784	657	HMMER 2.1.1	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	511.4	894	1835
			blastx.14	(AE000180) 7,8- diaminopelargonic acid synthetase [Escherichia coli]	gi 1786991 gb AAC7 3861.1	99% 100%	795 1837	1841 1860
HE9DG38	1181748	22	blastx.2	Putative selenocysteine lyase.	sp AAF36816 AAF36 816	99%	44	994
HE9DG38	943384	658	HMMER 2.1.1	PFAM: Aminotransferases class-	PF00266	215.1	160	1326

			blastx.14	V	similar to NIFS protein (nitrogen fixation) [Caenorhabditis elegans]	gi 722379 gb AAC46 685.1	45% 53% 61% 46% 41% 57% 41%	442 877 724 1210 1081 313 1379	678 1038 840 1344 1209 375 1450
HGBAT24	1024746	23	blastx.2		phosphoserine transaminase (EC 2.6.1.52) - Escherichia coli	pir B64830 B64830	97%	1	369
HGBAT24	761143	659	HMMER 2.1.1		PFAM: Aminotransferases class- V	PF00266	128.3	10	369
HTDAF92	1181747	24	blastx.2		CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO I	sp BAA91659 BAA9 1659	100%	256	1011
HTDAF92	943385	660	HMMER 2.1.1		PFAM: Aminotransferases class- V	PF00266	104.6	163	597
			blastx.2		(AF175767) putative selenocysteine lyase [Homo 1	gb AAF36816.1 AF1 75767_1	100%	160	627
HAPSI19	668405	25	HMMER 1.8		PFAM: Cytochrome C and Quinol oxidase polypeptide I	PF00115	75.81	263	382
			blastx.2		cytochrome-c oxidase (EC 1.9.3.1) chain I - human	pir A00463 ODHU1	76% 95%	3 263	263 382

HADTU18	666268	26	HMMER 1.8 blastx.2	mitochondrion PFAM: Cytochrome C oxidase subunit II cytochrome-c oxidase (EC 1.9.3.1) chain II - human mitochondrion	PF00116 pir A00472 OBHU2	50% 100% 99.8	28 385 185	87 399 307
HNTEF53	954852	27	HMMER 1.8 blastx.2	PFAM: Cytochrome P450 prostaglandin omega- hydroxylase (EC 1.14.15.-) cytochrome 1	PF00067 pir S32315 A29368	102.61 49% 42% 60%	369 821 279 1705	887 1714 902 1749
HWLLB11	954849	28	HMMER 1.8 blastx.2	PFAM: Cytochrome P450 CYTOCHROME P450 4C3 (EC 1.14.14.1) (CYP1VC3).	PF00067 sp Q9VA27 Q9VA27	159.13 46% 44%	75 78 4	506 512 75
HCRQK86	1193068	29	blastx.2	PROTEIN PHOSPHATASE 2C.	sp Q9Z1Z6 Q9Z1Z6	95%	164	1339
HCRQK86	918014	662	HMMER 2.1.1 blastx.14	PFAM: Protein phosphatase 2C (AF095927) protein phosphatase 2C [Rattus norvegicus]	PF00481 gi 3777604 gb AAC9 7497.1	248.4 89%	467 149	1297 1324
HOCOT88	933635	30	HMMER 2.1.1 blastx.2	PFAM: Protein phosphatase 2C protein phosphatase 2C- like protein - Arabidopsis thaliana	PF00481 pir T50783 T50783	196.9 38%	643 619	1350 1371
HELEF11	926930	31	HMMER	PFAM: Pyridoxal-	PF00282	202.9	146	565

		2.1.1	dependent decarboxylase conserved domain						
		blastx.2	glutamate decarboxylase (EC 4.1.1.15) beta - Escherichia coli		pir B43332 B43332	81% 100% 56% 47%	131 45 595 564	721 152 780 620	
HOUGD29	1204714	32	PANCREAS-ENRICHED PHOSPHOLIPASE C.		sp Q9UHV3 Q9UHV3	97% 79%	202 3	1821 203	
HOUGD29	909797	663	PFAM: Phosphatidylinositol-specific phospholipase C, Y domain		PF00387	118.2	202	453	
		blastx.14	(AF044576) phospholipase C PLC210 [Caenorhabditis elegans]		gi 2957270 gb AAC38963.1	42% 35% 58%	202 757 168	753 873 203	
HSIGN57	910078	33	PFAM: Phosphatidylinositol-specific phospholipase C, Y domain		PF00387	159.3	131	484	
		blastx.2	PHOSPHOLIPASE C-L2.		sp Q9QYG1 Q9QYG1	83%	2	754	
HTEPE35	948475	34	PFAM: Phosphatidylinositol-specific phospholipase C, Y domain		PF00387	163.8	839	507	
		blastx.2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase 1		pir S14113 S14113	48%	839	90	
HUFDB74	1227205	35	PHOSPHONOSITIDE-SPECIFIC		sp Q91423 Q91423	60%	2	547	

					PHOSPHOLIPASE C (FRAGMENT).					
HUFDB74	901451	664	HMMER 2.1.1		PFAM: Phosphatidylinositol- specific phospholipase C, Y domain	PF00387	89.4	2	127	
HBXAB33	1229908	36	blastx.2		growth/differentiation factor 5 - human	pir JC2347 JC2347	98%	54	581	
HBXAB33	957228	665	HMMER 2.1.1 blastx.14		PFAM: Aminotransferases class-I aspartate aminotransferase precursor (2.6.1.1) [Homo sapiens]	PF00155	663.4	2286	1081	
HMABF84	1198479	37	blastx.2		1- AMINOCYCLOPROPAN E-CARBOXILATE SYNTHASE.	gi 179104 gb AAA35 568.1	95%	2370	1081	
HMABF84	944629	666	HMMER 1.8 blastx.14		PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes]	sp Q9W698 Q9W698	54%	770	1462	
HPTVF17	1150836	38	blastx.2		1- AMINOCYCLOPROPAN E-CARBOXILATE SYNTHASE.	PF00155	37.62	55	429	
HPTVF17	936688	667	HMMER 1.8 blastx.2		PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes]	gi 4426837 gb AAD2 0564.1	58% 43%	1 452	447 499	
HPTVF17	936688	667	HMMER 1.8 blastx.2		PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes]	sp Q9W698 Q9W698	57% 59%	188 574	565 759	
HPTVF17	936688	667	HMMER 1.8 blastx.2		PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes]	PF00155	37.58	275	607	
HPTVF17	936688	667	HMMER 1.8 blastx.2		PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes]	gb AAD20564.1	52%	188	679	

HSDIC55	1197407	39	blastx.2	aminocyclopropane-carboxylate synthase [Fugu rubripes]	pir A00598 XNECD	96%	115	345
HSDIC55	506582	668	HMMER 1.8	PFAM: Aminotransferases class-I aspartate transaminase (EC 2.6.1.1) - Escherichia coli	PF00155	97.17	106	363
HSDIL35	1228138	40	blastx.2	aspartate transaminase (EC 2.6.1.1) - Escherichia coli	pir A00598 XNECD	98%	2	226
HSDIL35	656370	669	HMMER 2.1.1	PFAM: Aminotransferases class-I	PF00155	195.1	3	371
HTXSM05	1104951	41	blastx.2	alanine transaminase (EC 2.6.1.2), cytosolic - human	pir A40465 A40465	67% 70%	5 456	406 515
HTXSM05	958447	670	HMMER 1.8	PFAM: Aminotransferases class-I	PF00155	38.39	23	316
HYAAH23	1032585	42	blastx.14	alanine aminotransferase [Homo sapiens]	gi 1507680 dbj BAA01186.1	66%	5	358
HTPDX13	1134372	43	blastx.2	GLYOXYLATE REDUCTASE (EC 1.1.1.79)	sp Q9UBQ7 Q9UBQ7	92%	1	606
HTPDX13	948419	671	HMMER 1.8	CARBOXYPEPTIDASE X2	sp O54860 O54860	88%	2	922
HTPDX13	948419	671	blastx.14	PFAM: Zinc carboxypeptidases (AF017639)	PF00246	87.75	257	682
				carboxypeptidase X2 [Mus musculus]	gi 2921092 gb AAC04670.1	88%	2	922

HAIHE43	1172244	44	blastx.2	NEURONAL THREAD PROTEIN AD7C-NTP.	sp O60448 O60448	41%	2538	1981
HAIHE43	966830	672	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.22	275	322
HAJAV28	948630	45	HMMER 2.1.1	PFAM: Actin	PF00022	35.9	120	230
			blastx.2	Uncharacterized hypothalamus protein HARP11.	sp AAF67655 AAF67 655	97%	96	458
HAPOR59	712955	46	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	6.42	102	146
			blastx.2	CG5336 PROTEIN.	sp Q9VKB2 Q9VKB 2	40%	3	347
HBIBF78	772797	673	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.63	60	101
HCDAJ15	557243	674	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.61	68	88
HCE1S21	671209	49	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.17	163	210
			blastx.2	hypothetical protein F55G1.5 - Caenorhabditis elegans	pir T29225 T29225	60% 43%	41 224	124 292
HCE3J64	951228	50	HMMER 2.1.1	PFAM: Peptidase family M13	PF01431	154.1	234	563
			blastx.2	ENDOTHELIN-	sp O60344 ECE2_HU	94%	3	599

				CONVERTING ENZYME 2 (EC 3.4.24.71) (ECE-2) 1	MAN	59%	557	688
HCFCV92	934216	675	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.55	542	571
HCFLI54	921382	52	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	6.41	457	504
HCFND04	1155680	53	blastx.2	hypothetical protein ZK328.4 - <i>Caenorhabditis elegans</i>	pir T29006 T29006	28%	187	1134
HCFND04	873441	676	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.29	834	881
HCHMV63	666798	677	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.78	86	133
HCWDL45	889416	55	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.63	121	168
HCWEI19	1125258	56	blastx.2	alcohol dehydrogenase (EC 1.1.1.1) C - <i>Escherichia coli</i> (isolate VU 3685)	pir S57525 S57525	93%	215	436
HCWEI19	948690	678	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	8.6	226	273
			blastx.14	formaldehyde dehydrogenase (glutathione) [<i>Escherichia coli</i>]	gi 887431 emb CAA5 2057.1	75%	300	10
HCWKB72	1224131	57	blastx.2	SER/ARG-RELATED NUCLEAR MATRIX PROTEIN.	sp O60585 O60585	.67% 52% 100% 38%	2613 1482 2049 2637	2921 1808 2108 2744

HCWKB72	676007	679	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	29%	2613	2795
HDDAF49	1125713	58	blastx.2	hypothetical protein DKFZp434D0215.1 - human (fragment)	pir T42650 T42650	58% 33%	912 202	2613 2625 2616 2613 2631 2613 2613 2673 2860 2631
HDDAF49	911314	680	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain (AL133047) hypothetical protein [Homo sapiens]	PF00099	5.07	144	173
HDPGQ74	691163	59	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain TTYH1.	emb CAB61374.1 PF00099	52% 3.86	9 195	269 236
HDPGS68	752975	60	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain	sp AAG02580 AAG0 2580	44%	320	3
HDPX67	1172240	61	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain	PF00099	6.96	208	246
HDPX67	954385	681	HMMER 2.1.1	ORF2-LIKE PROTEIN (FRAGMENT).	sp O00549 O00549	37%	370	2
HDPX67	1172240	61	blastx.2	CDNA FLJ20378 FIS, CLONE KALA0536.	sp BAA91131 BAA9 1131	65% 60%	1936 2115	2124 2183
HDPX67	954385	681	HMMER 2.1.1	PFAM: Queuine tRNA- ribosyltransferase	PF01702	40.7	86	325

			blastx.14	(AE000733) queueine tRNA-ribosyltransferase [Aquifex aeolicus]	gi 2983726 gb AAC0 7288.1	35%	86	313
HDPXN01	915919	682	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.29	99	146
HDQFT77	1136137	63	blastx.2	KU70-BINDING PROTEIN (FRAGMENT)	sp Q9Y6H3 Q9Y6H3	95%	98	958
HDQFT77	932212	683	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	13.41	496	534
			blastx.14	(AF078164) Ku70- binding protein [Homo sapiens]	gi 4867999 gb AAD3 1085.1 AF078164_1	95%	13	873
HE2FR50	508498	64	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.68	137	166
			blastx.2	hypothetical protein DKFZp547N213.1 - human (fragment)	pir T50613 T50613	79%	122	355
HE2SN25	948687	684	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	9.04	227	268
HE8AE26	851514	685	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.8	49	75
HEBGK01	963673	67	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.13	426	391
			blastx.2	C380A1.2.1 (NOVEL PROTEIN (ISOFORM 1)).	sp Q9UJH9 Q9UJH9	81% 85% 100%	441 743 540	112 540 502
HEFMB30	691516	68	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.57	144	185
HEOPE58	851009	69	HMMER	PFAM: Zinc-binding	PF00099	5.32	320	364

				1.8	metallopeptase domain					
HETBR74	948667	70		HMMER 2.1.1	PFAM: Rhodanese-like domain	PF00581	32.2	321	461	
				blastx.2	DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC 1	sp O09112 DUS8_M OUSE	42% 54% 55%	291 458 535	476 523 588	
HFCAG94	1111177	71		blastx.2	PRO1722.	sp AAF69605 AAF69 605	66% 62%	860 1008	711 850	
HFCAG94	735763	686		HMMER 1.8	PFAM: Zinc-binding metallopeptase domain	PF00099	3.92	100	129	
HFPHR82	957528	72		HMMER 2.1.1	PFAM: Actin	PF00022	91.7	1322	357	
				blastx.2	Uncharacterized hypothalamus protein HARP11.	sp AAF67655 AAF67 655	100%	1523	273	
HHFO084	857780	73		HMMER 1.8	PFAM: Zinc-binding metallopeptase domain	PF00099	4.21	141	161	
HISAM68	1125189	74		blastx.2	CDNA FLJ20356 FIS, CLONE HEP15821.	sp BAA91112 BAA9 1112	100%	299	75	
HISAM68	868785	687		HMMER 1.8	PFAM: Zinc-binding metallopeptase domain	PF00099	3.48	178	198	
HLHDD45	942901	75		HMMER 1.8	PFAM: Zinc-binding metallopeptase domain	PF00099	5.88	177	218	
HMMAB49	1087684	76		blastx.2	CDNA FLJ20378 FIS, CLONE KAIA0536.	sp BAA91131 BAA9 1131	60% 80%	678 464	466 402	
HMMAB49	462502	688		HMMER 1.8	PFAM: Zinc-binding metallopeptase domain	PF00099	3.49	166	183	
HMSGO27	683031	77		blastx.2	Unnamed portein product.	sp BAB01630 BAB0 1630	57% 68%	77 295	238 369	

HMSGO27	943946	689	HMMER 2.1.1	PFAM: Reprolysin (M12B) family zinc metalloprotease	PF01421	59%	228	293
			blastx.2	(AF137335) metalloprotease disintegrin cysteine-rich protein, secreted form MDC-1s [Homo sapiens]	gb AAD25100.1	92% 98% 35%	232 18 2	462 245 103
HNHAM52	457010	691	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.5	72	89
HNHEQ86	785580	79	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.9	7	48
HNHFF46	859822	692	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.55	3	35
HOECV83	653276	693	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.67	360	389
HORBO54	870674	82	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.64	277	300
HOSFZ73	913876	694	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.29	335	355
HPIAU71	1123830	84	blastx.2	ethanolamine ammonia- lyase (EC 4.3.1.7) heavy chain - Escherichia coli (strain K-12)	pir H65018 H65018	98% 79% 38%	400 104 578	68 3 516
HPIAU71	786811	695	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.49	265	291
HRDBT72	1112136	85	blastx.2	PRO1722.	sp AAF69605 AAF69 605	73% 75% 57%	821 673 609	666 614 532

HRDBT72	507847	696	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	7.31	295	324
HSDFT51	1124582	86	blastx.2	AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) 1	sp O09175 AMPB_R AT	33%	1291	872
HSDFT51	947918	697	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	6.14	328	363
			blastx.14	aminopeptidase-B [Rattus norvegicus]	gi 1754515 dbj BAA1 3413.1	31% 36%	94 289	309 420
HSDJM56	948669	87	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	6.46	114	149
			blastx.2	formate C- acetyltransferase (EC 2.3.1.54) 1 - Escherichia coli	pir S01788 S01788	99% 99%	811 395	395 3
HSICX21	531267	88	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.8	307	336
HSIDS82	531248	89	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.91	206	238
HSNAH21	571314	90	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	7.14	91	135
HSODC08	966264	91	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	14.78	551	510
			blastx.2	BM-014.	sp AAF64270 AAF64 270	94%	779	222
HSPAB58	736098	92	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.6	39	86
HSQCM85	963554	93	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.37	187	231
HTOLA82	844319	94	HMMER	PFAM: Zinc-binding	PF00099	4.25	50	82

HUUDH57	931155	95	1.8 HMMER 2.1.1 blastx.2	metalloprotease domain PFAM: Peptidase family M1	PF01433	378.5	23	661
HWACV74	1145916	96	blastx.2	ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE. CDNA FLJ20378 FIS, CLONE KAIA0536.	sp Q9UKY2 Q9UKY 2	51%	2	2155
HWACV74	662347	698	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.43	198	242
HWAFW39	947915	97	HMMER 2.1.1 blastx.2	PFAM: Peptidase family M1	PF01433	79.5	200	367
HWBBR65	1156447	98	blastx.2	ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE. NEURONAL THREAD PROTEIN AD7C-NTP.	sp Q9UKY2 Q9UKY 2	96%	200	367
					sp O60448 O60448	48%	1246	866
						63%	1150	971
						54%	703	539
						78%	791	708
						50%	791	618
						55%	1113	985
						38%	840	532
						48%	994	803
						62%	2216	2130
						37%	995	753
						60%	682	614
						34%	703	560
						63%	2241	2176
						57%	767	711
						84%	2215	2177

								32%	972	796
HWBBR65	747723	699	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099			47%	1129	1061
HWMES65	969190	99	HMMER 2.1.1	PFAM: Matrixin	PF00413			46%	2183	2100
			blastx.2	HATCHING ENZYME PRECURSOR (EC 3.4.24.12) (HE) (HEZ) 1	sp P91953 HE_HEM PU		51%	606	532	
HISBG28	920850	100	HMMER 2.1.1	PFAM: 3'5'-cyclic nucleotide phosphodiesterase	PF00233		195.7	625	521	
			blastx.2	3'5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)	pir A47286 A47286		90%	2140	2099	
HAAJB60	786337	101	HMMER 2.1.1	PFAM: Aconitase family (aconitate hydratase)	PF00330		72.2	185	205	
			blastx.2	ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.3) (CITRATE HYDRO-LYASE) (ACONITASE).	sp Q99798 ACON_H UMAN		61%	17	109	
HDPDE32	1217181	102	blastx.2	aconitate hydratase (EC	pir G64875 G64875		91%	69	887	

HDPDE32	973342	700	HMMER 2.1.1	4.2.1.3) - Escherichia coli PFAM: Aconitase family (aconitate hydratase)	PF00330	260.7	219	569
HBDAC79	1199232	103	blastx.2	ACYL-COENZYME A DEHYDROGENASE-8 PRECURSOR (CDNA FLJ20352 FIS, CLONE HEP14524).	sp Q9UKU7 Q9UKU 7	86% 97% 45%	196 3 452	528 203 583
HBDAC79	935414	701	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	102.6	94	342
HEMDX48	1163778	104	blastx.2	(AL021958) fadE9 [Mycobacterium tuberculosis]	gi 2911026 emb CAA 17519.1	62% 51% 64% 35%	94 250 348 6	255 384 422 89
HEMDX48	521844	702	HMMER 1.8	PFAM: Acyl-CoA dehydrogenases	sp P50544 ACDV_M OUSE	48%	175	1917
HHASB48	721150	105	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	115.91	4	321
HLWCA17	1104762	106	blastx.2	probable acyl-CoA dehydrogenase PA2550 [imported] - Pseudomonas aeruginosa (strain PAO1)	sp P50544 ACDV_M OUSE	101.3	319	645
			blastx.2	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, 1	sp P50544 ACDV_M OUSE	54%	175	648
			blastx.2	probable acyl-CoA dehydrogenase PA2550 [imported] - Pseudomonas aeruginosa (strain PAO1)	sp P50544 ACDV_M OUSE	62%	359	979

HLWCA17	957664	703	HMMER 1.8	PFAM: Acyl-CoA dehydrogenases	PF00441	52.61	521	892
			blastx.14	(AL096811) putative acyl-CoA dehydrogenase [Streptomyces coelicolor A3(2)]	gi 5441764 emb CAB46788.1	53% 58%	521 286	904 519
HNTTD09	1104487	107	blastx.2	K09H11.1 PROTEIN.	sp O01590 O01590	47% 32%	179 6	832 152
HNTTD09	676665	704	HMMER 1.8	PFAM: Acyl-CoA dehydrogenases	PF00441	49.76	60	425
HSKDT07	927823	108	HMMER 1.8	PFAM: Acyl-CoA dehydrogenases	PF00441	122.42	13	369
			blastx.2	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, 1	sp P50544 ACDV_M OUSE	38%	7	906
HSRDB26	1102231	109	blastx.2	acyl CoA dehydrogenase homolog - Escherichia coli	pir I41124 I41124	99% 72% 81%	305 27 2	658 305 34
HSRDB26	525475	705	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	115.7	21	290
HAPBS07	967325	110	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	50.05	61	267
			blastx.2	RETINOL DEHYDROGENASE HOMOLOG.	sp Q9Y2P9 Q9Y2P9	75% 69% 62% 34%	317 61 580 561	682 306 708 683
HAUAI17	921674	111	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	198.7	172	687

			blastx.2	RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSDR3.	sp Q9UKU3 Q9UKU3	81% 100%	145 687	687 857
HBCBT19	95953	112	HMME 2.1.1 blastx.2	PFAM: short chain dehydrogenase hypothetical protein F17A8.100 - Arabidopsis thaliana	PF00106 pir T04022 T04022	30.7 40% 41% 52%	202 214 38 591	417 552 196 653
HBCPT10	957631	113	HMME 1.8 blastx.2	PFAM: Alcohol/other dehydrogenases, short chain type CDNA FLJ11008 FIS, CLONE PLACE1003100, MODERATELY SIMILAR 1	PF00106 sp BAA91953 BAA91953	98.87 97% 80%	338 263 671	673 670 838
HBGDA14	866258	114	HMME 1.8 blastx.2	PFAM: Alcohol/other dehydrogenases, short chain type 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28) - Escherichia coli	PF00106 pir A91904 DEECDB	127.15 92%	3 3	299 482
HCHNJ32	934848	115	HMME 2.1.1 blastx.2	PFAM: short chain dehydrogenase CARBONYL REDUCTASE.	PF00106 sp Q9UHY9 Q9UHY9	213.6 95%	54 33	587 764
HCHON59	931082	116	HMME 2.1.1	PFAM: SCP-2 sterol transfer family	PF02036	96.3	1006	1335

			blastx.2	CG5590 PROTEIN.	sp Q9VB10 Q9VB10	47%	538	1344
HCUGN19	716989	117	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	68%	99	536
HCUGR38	706471	118	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	73.02	102	284
			blastx.2	Putative oxidoreductase.	sp CAB94622 CAB9 4622	55% 30%	105 4	296 81
HDPND85	852628	119	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	191.2	113	709
			blastx.2	CG9360 PROTEIN.	sp Q9VYU9 Q9VYU 9	42%	113	841
HDPRN38	883658	120	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	175.59	123	680
			blastx.2	Peroxisomal trans 2-enoyl CoA reductase (EC 1.3.1.8).	sp AAF69798 AAF69 798	81% 84%	111 61	824 138
HE8AM92	952610	121	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	8.98	202	330
			blastx.2	DTDP-4-KETO-6- DEOXY-D-GLUCOSE 4- REDUCTASE.	sp Q9UI54 Q9UI54	90%	208	654
HE9RE21	888243	122	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	81.3	96	386
			blastx.2	ESTRADIOL 17 BETA-	sp P56937 DHB7_H	100%	90	419

				DEHYDROGENASE 7 (EC 1.1.1.62) 1	UMAN	88%	421	522
HETKH30	884009	123	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	137.09	300	881
			blastx.2	PUTATIVE STERIOD DEHYDROGENASE SPM2 (EC 1.1.1.-).	sp O57314 DHBX_A NAPL	54%	294	866
HHAME78	840939	124	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	55.01	60	260
			blastx.2	CARBONYL REDUCTASE.	sp Q9UHY9 Q9UHY 9	83% 100% 95% 81%	48 322 257 2	260 426 322 67
HKABI68	856590	125	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	11.34	109	285
			blastx.2	HSCARG.	sp AAG09721 AAG0 9721	99% 75%	139 456	441 551
HKMLN95	914083	126	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	100.69	23	361
			blastx.2	STERIOD DEHYDROGENASE HOMOLOG.	sp Q9Y6G8 Q9Y6G8	98%	20	583
HMCFA91	959954	127	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	25.77	19	282
			blastx.2	hypothetical protein	pir T04022 T04022	53%	367	648

				F17A8.100 - Arabidopsis thaliana		41%	1	282
HNTBF75	836701	128	HMMER 2.1.1 blastx.2	PFAM: short chain dehydrogenase	PF00106	35.2	202	321
				STEROID DEHYDROGENASE HOMOLOG.	sp Q9Y6G8 Q9Y6G8	78%	52	414
HPTGB43	726460	129	HMMER 2.1.1 blastx.2	PFAM: short chain dehydrogenase	PF00106	45.1	84	191
				CARBONYL REDUCTASE.	sp Q9UHY9 Q9UHY 9	73%	87	374
HPTVL90	509487	130	HMMER 2.1.1 blastx.2	PFAM: short chain dehydrogenase	PF00106	46.3	11	115
				RETINAL SHORT- CHAIN DEHYDROGENASE/RE DUCTASE RETSDR3.	sp Q9UKU3 Q9UKU 3	76%	8	319
HSKIA89	837986	131	HMMER 1.8 blastx.2	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	17.7	359	478
				hypothetical protein T11F9.11 - Caenorhabditis elegans	pir T24832 T24832	42% 53% 35%	329 123 737	619 320 820
HTXGF27	695766	132	HMMER 2.1.1 blastx.2	PFAM: short chain dehydrogenase	PF00106	208.7	193	765
				hypothetical protein DKFZp566O084.1 - human	pir T17307 T17307	93% 100%	70 38	1011 73
HWHHW54	684125	133	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	59.1	871	1002

			blastx.2	Oxidoreductase UCPA.	sp AAF80754 AAF80754.	77%	871	1059
HWHPO29	857383	134	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	101.3	257	664
			blastx.2	CGI-82 PROTEIN.	sp Q9Y391 Q9Y391	74% 64%	257 186	664 260
HWLPR94	967326	135	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	44.2	193	417
			blastx.2	RETINOL DEHYDROGENASE HOMOLOG.	sp Q9Y2P9 Q9Y2P9	95% 84%	184 36	450 134
HWLJL28	925331	136	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	113.24	163	588
			blastx.2	C359F1.1 (novel protein (ortholog of mouse and rat 1	sp CAB92744 CAB92744	82%	97	735
HWLXT48	957630	137	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	46.57	133	306
			blastx.2	CDNA FLJ11008 FIS, CLONE PLACE1003100, MODERATELY SIMILAR 1	sp BAA91953 BAA91953	83% 94%	58 309	333 359
HBGMD15	1103922	138	blastx.2	L-threonine 3-dehydrogenase (EC 1.1.1.103) - Escherichia coli	pit A33276 DEECTH	91% 79%	64 554	564 655
			HMMER	PFAM: Zinc-binding	PF00107	141.1	3	323
HBGMD15	786307	706	HMMER					

HNGMA91	789744	139	2.1.1 HMMER 1.8	dehydrogenases PFAM: Zinc-binding dehydrogenases	PF00107	28.74	76	231
			blastx.2	probable alcohol dehydrogenase (EC 1.1.1.1) ybdR - Escherichia coli	pir F64794 F64794	92%	76	318
HSLEI57	1103672	140	blastx.2	alcohol dehydrogenase (EC 1.1.1.1) C - Escherichia coli	pir D64763 D64763	87%	74	565
HSLEI57	730927	707	HMMER 2.1.1	PFAM: Zinc-binding dehydrogenases	PF00107	236	5	388
HSLFE21	1103524	141	blastx.2	probable oxidoreductase (EC 1.1.1.-) ycjQ - Escherichia coli	pir D64880 D64880	95%	2	994
HSLFE21	823083	708	HMMER 1.8	PFAM: Zinc-binding dehydrogenases	PF00107	76.21	344	655
HSLIE40	1105422	142	blastx.2	probable alcohol dehydrogenase (EC 1.1.1.1) ybdR - Escherichia coli	pir F64794 F64794	97%	88	510
HSLIE40	866274	709	HMMER 1.8	PFAM: Zinc-binding dehydrogenases	PF00107	30.97	152	283
HTXHA35	1152110	143	blastx.2	CGI-63 PROTEIN.	sp Q9Y373 Q9Y373	98% 72%	309 14	836 190
HTXHA35	633682	710	HMMER 1.8	PFAM: Zinc-binding dehydrogenases	PF00107	53.56	265	471
HAICS07	1105538	144	blastx.2	ALDO-KETO REDUCTASE.	sp O09125 O09125	75% 75% 63%	193 535 733	480 738 798

HAICS07	953351	711	HMMER 2.1.1 blastx.14	PFAM: Aldo/keto reductase family aldo-keto reductase [Mus musculus]	PF00248	283	193	480
HBKDN33	1167313	145	blastx.2	Acetyl-CoA synthetase.	sp AAF75064 AAF75 064	85% 85%	2 955	1015 1014
HBKDN33	922414	712	HMMER 2.1.1 blastx.14	PFAM: AMP-binding enzyme acetyl-CoA synthetase [Drosophila melanogaster]	PF00501	249.5	2	931
HBODH62	1228278	146	blastx.2	DJ568C11.3 (novel AMP- binding enzyme similar to 1	gi 608694 emb CAA8 6738.1 sp CAB75500 CAB7 5500	98% 100%	344 297	1696 362
HBODH62	742827	713	HMMER 1.8 blastx.2	PFAM: AMP-binding enzymes	PF00501	43.02	27	158
HCEPJ44	1157810	147	blastx.2	Sequence 17 from Patent WO951740.	sp CAC07591 CAC0 7591	99%	2	571
HCEPJ44	930790	714	HMMER 1.8 blastx.14	PFAM: AMP-binding enzymes (AF023258) fatty acid transport protein [Mus musculus]	PF00501	19.17	3	215
HCWCM65	1105668	148	blastx.2	probable non-ribosomal peptide synthetase PA2402 [imported] - Pseudomonas aeruginosa (strain PAO1)	gi 2612939 gb AAC6 9640.1 pir F83345 F83345	90% 75% 74% 37% 31% 57% 53%	9 12 12 9 9 595 595	536 611 611 605 596 678 678
HCWCM65	529230	715	HMMER	PFAM: AMP-binding	PF00501	69.62	31	264

HDQDY52	1182322	149	1.8 blastx.2	enzymes DJ18C9.1 (SIMILAR TO ACETYL-COENZYME A SYNTHETASE) 1	sp Q9UJ15 Q9UJ15	84% 81% 55%	85 566 705	690 778 785
HDQDY52	852622	716	HMMER 1.8 blastx.2	PFAM: AMP-binding enzymes (AL049709) dJ18C9.1 (similar to acetyl- coenzyme A synthetase) [Homo sapiens]	PF00501 emb CAB61786.1	82.8 84% 81% 55%	316 85 566 705	555 690 778 785
HEEAA32	1203140	150	blastx.2	CDNA FLJ20581 FIS, CLONE REC00491.	sp BAA91273 BAA9 1273	93% 97% 57%	502 3 1146	1182 500 1208
HEEAA32	887490	717	HMMER 1.8	PFAM: AMP-binding enzymes	PF00501	35.92	39	407
HEGAN70	839719	151	HMMER 1.8 blastx.2	PFAM: AMP-binding enzymes Hypothetical 179.7 kDa protein.	PF00501 sp AAF64300 AAF64 300	18.6 61% 85% 34% 54%	334 124 31 295 748	516 654 111 579 846
HFKMF42	1104119	152	blastx.2	Long-chain-fatty-acid- CoA ligase-like protein.	sp BAB02683 BAB0 2683	48% 41%	656 65	1096 556
HFKMF42	923824	718	HMMER 1.8 blastx.14	PFAM: AMP-binding enzymes 4-coumarate-coA ligase [Mycobacterium leprae]	PF00501 gi 699196 gb AAA62 961.1	91.1 51% 48% 55% 36% 50%	86 764 647 365 968 491	901 949 781 484 1099 568

HFPHG06	1104964	153	blastx.2	enterobactin synthetase component F - Escherichia coli	pir H64791 YGECEF	53% 44%	65 570	103 623
HFPHG06	933802	719	HMMER 2.1.1 blastx.14	PFAM: AMP-binding enzyme enterobactin [Escherichia coli]	PF00501 gi 145843 gb AAA92015.1	66 90%	53 2	232 220
HHEMB89	1227613	154	blastx.2	DJ568C11.3 (novel AMP-binding enzyme similar to 1	sp CAB75500 CAB75500	99%	561	1961
HHEMB89	574897	720	HMMER 2.1.1	PFAM: AMP-binding enzyme	PF00501	115.4	1	453
HLDPC46	466567	155	HMMER 1.8 blastx.2	PFAM: AMP-binding enzymes CDNA FLJ20581 FIS, CLONE REC00491.	PF00501 sp BAA91273 BAA91273	103.84 89% 57%	17 586	481 571 681
HLDRG44	1106225	156	blastx.2	KIDNEY-SPECIFIC PROTEIN.	sp O70490 O70490	74%	16	1011
HLDRG44	969544	721	HMMER 1.8 blastx.14	PFAM: AMP-binding enzymes (AF062389) kidney-specific protein [Rattus norvegicus]	PF00501 gi 3127193 gb AAD05209.1	104.64 78%	89 2	694 931
HLICR73	1107517	157	blastx.2	VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 2.	sp Q9Y2P5 Q9Y2P5	96%	9	536
HLICR73	837030	722	HMMER	PFAM: AMP-binding	PF00501	20.33	19	324

			1.8 blastx.2	enzymes (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	gb AAD29444.1 AF064255_1	99% 100%	1 450	441 497
HNHOP64	1103943	158	blastx.2	FATTY ACID TRANSPORT PROTEIN.	sp O95186 O95186	90% 52%	515 57	57 1
HNHOP64	966754	723	HMMER 1.8 blastx.14	PFAM: AMP-binding enzymes (AF055899) fatty acid transport protein [Homo sapiens]	PF00501 gi 4206376 gb AAD11623.1	23.65% 88% 52%	539 374 835	757 835 891
HSDEF56	1128288	159	blastx.2	acetate--CoA ligase (EC 6.2.1.1) - Escherichia coli	pir D65215 D65215	97% 95% 100%	106 707 897	729 892 986
HSDEF56	496551	724	HMMER 2.1.1	PFAM: AMP-binding enzyme	PF00501	175.3	2	436
HTENI29	1105518	160	blastx.2	LONG-CHAIN ACYL-COA SYNTHETASE 5.	sp Q9UKU0 Q9UKU0	97%	24	1172
HTENI29	954519	725	HMMER 1.8 blastx.14	PFAM: AMP-binding enzymes (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]	PF00501 gi 5702202 gb AAD47199.1 AF129166_1	65% 98%	366 51	845 1172
HWMKD72	1106729	161	blastx.2	agmatinase PA1421 [imported] - Pseudomonas aeruginosa (strain PAO1)	pir H83468 H83468	64%	2	643
HWMKD72	970613	726	HMMER 2.1.1 blastx.14	PFAM: Arginase family agmatine ureohydrolase	PF00491 gi 82466 gb AAA69	179.6% 48%	11 302	565 625

					[Escherichia coli]	104.1		50%	14	166
HAPSQ21	972037	162	HMMER 2.1.1		PFAM: Eukaryotic aspartyl protease	PF00026		44%	164	271
			blastx.2		NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A) (NAPA) 1	sp O96009 NAP1_H UMAN		274.4	211	735
HLJDW02	1192885	163	blastx.2		NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A) (NAPA) 1	sp O96009 NAP1_H UMAN		100% 90%	58 767	762 865
HLJDW02	837592	727	HMMER 2.1.1 blastx.2		PFAM: Eukaryotic aspartyl protease (AF090386) napsin A [Homo sapiens]	PF00026		134.5	65	412
HMGBT01	1205666	164	blastx.2		aspartic proteinase (EC 3.4.23.-) BACE precursor - human	gb AAD04917.1		100% 65%	47 433	433 534
HMGBT01	879904	728	HMMER 1.8		PFAM: Eukaryotic aspartyl proteases	PF00026		31.46	3	362
HSSJJ24	1178041	165	blastx.2		aspartic proteinase (EC 3.4.23.-) BACE precursor - human	pir A59090 A59090		100% 85%	8 1714	1081 2001
HSSJJ24	905092	729	HMMER 1.8		PFAM: Eukaryotic aspartyl proteases	PF00026		26.48	33	113
HFTCG46	669383	166	HMMER 2.1.1 blastx.2		PFAM: Eukaryotic-type carbonic anhydrase	PF00194		101.7	78	266
					CARBONIC ANHYDRASE VB, MITOCHONDRIAL PRECURSOR (EC 1	sp Q9Y2D0 CA5B_H UMAN		98%	78	257

HNTMD81	929511	167	HMMER 2.1.1 blastx.2	PFAM: Eukaryotic-type carbonic anhydrase CARBONIC ANHYDRASE XIV PRECURSOR (EC 4.2.1.1) (CARBONATE 1 OUTER MEMBRANE USHER PROTEIN PMFC PRECURSOR.	PF00194 sp Q9ULX7 CAHE_ HUMAN	84.3	16	249
HBSAJ60	1174334	168	blastx.2	PFAM: Citrate synthase	sp Q9R7S7 Q9R7S7	99% 97%	2043 2888	2885 3331
HBSAJ60	573965	730	HMMER 2.1.1	PFAM: Citrate synthase	PF00285	192	2	265
HSKCI43	506599	169	HMMER 1.8 blastx.2	PFAM: Citrate synthase	PF00285	69.36	1	315
HSDKE47	1128095	170	blastx.2	citrate (si)-synthase (EC 4.1.3.7) - Escherichia coli NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUFS2 precursor - human	pir G64807 YKEC pir JE0193 JE0193	64% 96% 100%	1 168 73	345 260 195
HSDKE47	764970	731	HMMER 2.1.1	PFAM: Respiratory-chain NADH dehydrogenase, 49 Kd subunit	PF00346	79.8	64	195
HCWTB56	1172460	171	blastx.2	probable cation- transporting P-type ATPase PA2435 [imported] - Pseudomonas aeruginosa (strain PAO1)	pir F83342 F83342	65% 95%	2 270	268 332
HCWTB56	853009	732	HMMER 1.8 blastx.2	PFAM: E1-E2 ATPases	PF00122	55.15	2	301
				cadmium resistance	gb AAB37345.1	42%	2	316

HFPBS73	1144027	172	blastx.2	protein [Lactococcus lactis] H+/K+-exchanging ATPase (EC 3.6.1.36) chain B [validated] - Escherichia coli	pir H64804 PWECB K	81%	373	1122
HFPBS73	954892	733	HMMER 2.1.1 blastx.2	PFAM: E1-E2 ATPase kdpB [Escherichia coli]	PF00122 gb AAB96336.1	196.5 100% 100%	3 580	572 563 603
HOEDD44	954893	173	HMMER 2.1.1 blastx.2	PFAM: E1-E2 ATPase H+/K+-exchanging ATPase (EC 3.6.1.36) chain B [validated] - Escherichia coli	PF00122 pir H64804 PWECB K	173.2 92% 96% 39%	53 53 634 513	574 574 723 635
HSUAN33	956315	174	HMMER 1.8 blastx.2	PFAM: E1-E2 ATPases Hypothetical 128.8 kDa protein.	PF00122 sp CAB89728 CAB8 9728	46.29 48% 35%	1317 1596 693	907 766 256
HBCMD49	1206021	175	blastx.2	hypothetical protein F38H4.8 - Caenorhabditis elegans	pir T21981 T21981	44%	46	357
HBCMD49	865314	734	HMMER 2.1.1 blastx.2	PFAM: Enoyl-CoA hydratase/isomerase family (AE000989) enoyl-CoA hydratase (fad-4) [Archaeoglobus fulgidus]	PF00378 gb AAB89601.1	74.6 39%	263 197	550 619
HKABN12	956826	176	HMMER	PFAM: Enoyl-CoA	PF00378	31.8	900	820

			2.1.1	hydratase/isomerase family						
			blastx.2	CG6984 PROTEIN.	sp Q9V7Y3 Q9V7Y3	37%	745	593		
						41%	891	739		
HMOAC31	1228291	177	blastx.2	probable 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) ydbU - Escherichia coli (strain K-12)	pir F64890 F64890	93%	1297	2586		
HMOAC31	920386	735	HMMER 2.1.1	PFAM: Enoyl-CoA hydratase/isomerase family	PF00378	159.1	5	268		
			blastx.14	enoyl-CoA hydratase [Escherichia coli]	gi 2764828 emb CAA66095.1	88%	2	355		
						90%	334	495		
HMVBO92	1204710	178	blastx.2	CDNA FLJ10948 FIS, CLONE PLACE1000142, WEAKLY SIMILAR TO 1	sp BAA91922 BAA91922	99%	1701	2090		
HMVBO92	791284	736	HMMER 1.8	PFAM: Enoyl-CoA hydratase/isomerase	PF00378	32.87	167	274		
HOELA62	1228151	179	blastx.2	CDNA FLJ10948 FIS, CLONE PLACE1000142, WEAKLY SIMILAR TO 1	sp BAA91922 BAA91922	98%	1685	2074		
HOELA62	863712	737	HMMER 2.1.1	PFAM: Enoyl-CoA hydratase/isomerase family	PF00378	39.5	1635	1757		
HSSGE35	1228152	180	blastx.2	CDNA FLJ10948 FIS, CLONE PLACE1000142,	sp BAA91922 BAA91922	89%	97	498		

					WEAKLY SIMILAR TO 1					
HSSGE35	967832	738	HMMER 1.8		PFAM: Enoyl-CoA hydratase/isomerase	PF00378	39.59	70	210	
			blastx.14		AU-binding protein/Enoyl-CoA hydratase [Homo sapiens]	gi 780241 emb CAA5 6260.1	57% 55% 69%	88 1 363	357 87 401	
HEMF174	1216651	181	blastx.2		GLUCOSAMINE-- FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE 11	sp O94808 GFA2_H UMAN	100% 98%	193 1301	1299 1468	
HEMF174	523350	739	HMMER 2.1.1		PFAM: Glutamine amidotransferases class-II	PF00310	74.1	124	348	
HISCL24	676997	182	HMMER 2.1.1		PFAM: Glutamine amidotransferases class-II	PF00310	92.7	3	233	
			blastx.2		GLUCOSAMINE-- FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE 11	sp O94808 GFA2_H UMAN	85%	3	560	
H7PBB83	1228150	183	blastx.2		CG9630 PROTEIN.	sp Q9VHU1 Q9VHU 1	47% 56% 25%	145 955 776	774 1044 871	
H7PBB83	908235	740	HMMER 1.8		PFAM: Helicases conserved C-terminal domain	PF00271	84.64	756	586	
			blastx.14		(AJ010469) RNA helicase [Arabidopsis thaliana]	gi 3776011 emb CAA 09208.1	54% 49%	756 516	514 310	
HAGBA63	1122199	184	blastx.2		PUTATIVE ATP-	sp O43630 O43630	99%	1121	78	

					DEPENDENT MITOCHONDRIAL RNA HELICASE.				
HAGBA63	509775	741	HMMER 1.8		PFAM: Helicases conserved C-terminal domain	PF00271	7.62	2	124
HBMUG47	1102698	185	blastx.2		RECQ HELICASE 5 (DNA HELICASE RECQ5 GAMMA).	sp Q9UNC8 Q9UNC 8	98%	21	530
HBMUG47	863846	742	HMMER 1.8		PFAM: Helicases conserved C-terminal domain	PF00271	52.06	22	204
HCRPZ84	1130816	186	blastx.2		RNA helicase.	sp AAG09428 AAG0 9428	37% 25% 34% 40%	3 1469 1161 834	893 1942 1640 1013
HCRPZ84	965476	743	HMMER 1.8 blastx.14		PFAM: Helicases conserved C-terminal domain (AF038963) RNA helicase [Homo sapiens]	PF00271 gi 4405795 gb AAD1 9826.1	13.09 45% 43% 59% 50% 56% 45% 30% 44%	923 137 506 26 1063 413 863 737 1154	1063 373 622 91 1140 460 934 853 1228
HCWTR54	1192287	187	blastx.2		NEURONAL THREAD PROTEIN AD7C-NTP.	sp O60448 O60448	64% 69% 48%	304 245 313	179 120 233

HCWTR54	729290	744	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	27%	331	233
HDPBB41	1195686	188	blastx.2	RNA helicase HEL117 - rat	pir A57514 A57514	85%	364	344
HDPBB41	925800	745	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	6.14	151	198
HEOPI32	907903	189	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	90%	2411	564
HFSAG03	1151479	190	blastx.2	(AF106680) RNA helicase [Homo sapiens]	gi 5410326 gb AAD4 3033.1	88%	2722	2372
HFSAG03	960973	746	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	45%	2814	2545
HFXCI24	1182719	191	blastx.2	DJ620E11.1A (NOVEL HELICASE C- TERMINAL DOMAIN AND SNF2 1 1	sp Q9UJF0 Q9UJF0	108.7	47	292
HFXCI24	908374	747	HMMER 2.1.1	probable ATP-dependent RNA helicase rhIE - Escherichia coli	pir E64816 E64816	82%	17	637
HFXCI24	908374	747	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	89.44	176	430
HFXCI24	908374	747	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	87%	2	661
HFXCI24	908374	747	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	67%	967	1086
HFXCI24	908374	747	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	6.39	454	365
HFXCI24	908374	747	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	81%	12	674
HFXCI24	908374	747	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	128.5	151	396

			blastx.14	Putative ATP-dependent RNA helicase RhlE. [Escherichia coli]	gi 4062355 dbj BAA35457.1	94% 100%	1 644	543 664
HFXHJ89	907938	192	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	88.81	216	470
			blastx.2	DJ620E11.1A (NOVEL HELICASE C-TERMINAL DOMAIN AND SNF2 1 1	sp Q9UJF0 Q9UJF0	98% 78% 48%	210 37 5	881 207 85
HHPTC55	1106390	193	blastx.2	hypothetical protein C27B7.4 - Caenorhabditis elegans	pir T19508 T19508	47%	2	541
HHPTC55	907951	748	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	61.91	13	243
			blastx.14	(AF026032) ATRX protein [Mus musculus]	gi 3002558 gb AAC08741.1	54%	4	351
HJBBP54	1195070	194	blastx.2	DJ616B8.1 (RNA HELICASE) (Fragment).	sp CAC03449 CAC03449	89%	3	551
HJBBP54	869621	749	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	10.61	3	170
			blastx.2	(AC005314) putative pre-mRNA splicing factor RNA helicase [Arabidopsis thaliana]	gb AAC36188.1	54%	3	563
HKAHB56	1162649	195	blastx.2	RNA helicase.	sp AAG09428 AAG09428	28% 31% 33%	833 333 54	1606 824 389

HKAHB56	865298	750	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	63.37	699	986
HLDCI35	1151490	196	blastx.2	APOBEC-1 stimulating protein.	sp CAB94754 CAB9 4754	83%	84	725
HLDCI35	831356	751	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	6.01	288	374
			blastx.2	(AF209192) Apobec-1 complementation factor [Homo 1	gb AAF34824.1 AF2 09192_1	94%	177	725
HMCBU79	1165318	197	blastx.2	CDNA FLJ20110 FIS, CLONE COL05103.	sp BAA90955 BAA9 0955	89%	1	987
HMCBU79	856630	752	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	17.95	349	459
HNTRV07	1199546	198	blastx.2	Cytoplasmic dynein heavy chain.	sp BAA97048 BAA9 7048	92% 91% 40%	934 18 48	2001 923 152
HNTRV07	952794	753	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	6.41	274	345
			blastx.14	similar to dynein heavy chain; cDNA EST EMBL:D27549.1 [Caenorhabditis elegans]	gi 3876099 emb CAA 99830.1	33%	46	333
HODEX10	926260	754	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	9.2	22	54
HOGAQ10	1222600	200	blastx.2	Proliferation-associated	sp AAF82262 AAF82	99%	1045	1992

HOGAQ10	907911	755			SNF2-like protein. PFAM: Helicases conserved C-terminal domain	262		94%	98	1051
				HMMER 1.8		PF00271		47.76	80	178
HOSBW20	985056	201		blastx.14	lymphocyte specific helicase [Mus musculus]	gi 805296 gb AAB08 015.1		93%	80	556
HOSBW20	668774	756		blastx.2 HMMER 1.8	CG7972 PROTEIN. PFAM: Helicases conserved C-terminal domain	sp Q9VSE2 Q9VSE2 PF00271		83% 47%	18 4	71 777
HRADL60	1151310	202		blastx.2	probable pre-mRNA splicing factor ATP- dependent RNA helicase - fission yeast (Schizosaccharomyces pombe)	pir T37496 T37496		40% 42%	2750 2750	1416 1737
HRADL60	967578	757		HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271		14.84	248	496
				blastx.2	(AL009197) putative pre- mRNA splicing factor ATP-dependent RNA helicase [Schizosaccharomyces pombe]	emb CAA15715.1		40% 44%	83 83	1429 1096
HSGSC29	1150837	203		blastx.2	ACTIN INTERACTING PROTEIN.	sp O23240 O23240		56%	334	750
HSGSC29	953599	758		HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271		9.31	345	446

			blastx.14	actin interacting protein [Arabidopsis thaliana]	gi 4006920 emb CAB 16815.1	53%	468	740
HTEDX38	1106208	204	blastx.2	DEAD-BOX PROTEIN.	sp Q9Y659 Q9Y659	70%	333	452
HTEDX38	920697	759	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	90%	55	1494
			blastx.14	(AF106019) DEAD-box protein [Homo sapiens]	gi 5359631 gb AAD4 2744.1 AF106019_1	90%	3	176
HTEJE15	1102531	205	blastx.2	VASA protein.	sp AAF72705 AAF72 705	100%	1	405
HTEJE15	908360	760	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	14.92	5	52
			blastx.14	vasa-like gene protein, RVLG protein=putative DEAD 1 [Rattus sp.]	gi 806464 gb AAB33 364.1	73% 84% 65%	2 242 188	190 319 265
HTOES03	1150877	206	blastx.2	TRANSCRIPTIONAL ACTIVATOR SRCAP.	sp Q9Y5L9 Q9Y5L9	40%	203	1186
HTOES03	955814	761	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	53.97	240	491
			blastx.14	(AF143946) transcriptional activator SRCAP [Homo sapiens]	gi 5106572 gb AAD3 9760.1 AF143946_1	50% 39% 33%	6 906 540	569 1019 656
HTOHS18	1193057	207	blastx.2	ATP-DEPENDENT RNA HELICASE.	sp Q9SHB9 Q9SHB9	39%	39	857
HTOHS18	908347	762	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	104.65	158	370
			blastx.14	(AC007660) putative	gi 4895231 gb AAD3	45%	23	439

					RNA helicase [Arabidopsis thaliana]	2817.1 AC007660_18	47%	579	761
HWAAX38	943936	208	HMMER 1.8		PFAM: Helicases conserved C-terminal domain	PF00271	34.57	48	221
			blastx.2		PUTATIVE SNF2/SW12 FAMILY TRANSCRIPTION FACTOR.	sp Q9SHB2 Q9SHB2	46%	39	380
HMSFN70	1210794	209	blastx.2		CDNA FLJ20421 FIS, CLONE KAT02467.	sp BAA91158 BAA9 1158	96%	1	921
HMSFN70	921879	763	HMMER 2.1.1		PFAM: Inositol monophosphatase family	PF00459	40.2	703	795
			blastx.14		(AL032655) predicted using Genefinder; similar to 1 this gene [Caenorhabditis elegans]	gi 3881275 emb CAA 21725.1	43%	328	492
HUSGB93	1224029	210	blastx.2		BISPHOSPHATE 3'- NUCLEOTIDASE.	sp O95861 O95861	99%	426	953
HUSGB93	923014	764	HMMER 1.8		PFAM: Inositol monophosphatase family	PF00459	100%	146	364
			blastx.14		(AF125042) bisphosphate 3-nucleotidase [Homo sapiens]	gi 4325316 gb AAD1 7329.1	33.91	125	388
HELHL56	1164004	211	blastx.2		CDNA FLJ11068 FIS, CLONE PLACE1004918, WEAKLY SIMILAR TO 1	sp BAA91985 BAA9 1985	100%	17	493
HELHL56	578441	765	HMMER 1.8		PFAM: L-lactate dehydrogenases	PF00056	99%	8	655
							33.17	80	211

HOENY85	1191756	212	blastx.2	CDNA FLJ11068 FIS, CLONE PLACE1004918, WEAKLY SIMILAR TO 1	sp BAA91985 BAA9 1985	93%	53	1069
HOENY85	875830	766	HMMER 1.8	PFAM: L-lactate dehydrogenases	PF00056	144.25	38	598
HTEHI14	1102680	213	blastx.2	LACTATE DEHYDROGENASE A (EC 1.1.1.27).	sp Q9XT87 Q9XT87	68%	218	523
HTEHI14	526687	767	HMMER 2.1.1	PFAM: lactate/malate dehydrogenase	PF00056	50.6	222	371
HETDT70	1228235	214	blastx.2	NMD PROTEIN.	sp O95991 O95991	99% 52%	25 540	558 596
HETDT70	937999	768	HMMER 2.1.1	PFAM: Lipase	PF00151	125.4	139	528
			blastx.2	similar to the following EST sequences: GenBank Accession 1 sapiens]	gb AAC99994.1	88% 52%	25 539	597 595
HPIAT34	936262	215	HMMER 2.1.1	PFAM: Lipase	PF00151	123.9	305	535
			blastx.2	NMD PROTEIN.	sp O95991 O95991	80% 100% 92% 66%	266 84 12 277	574 275 95 330
HDPPO41	1204324	216	blastx.2	malate dehydrogenase (NAD+) (EC 1.1.1.-) precursor, mitochondrial - human	pir A39503 A39503	98%	186	1937
HDPPO41	963126	769	HMMER 2.1.1	PFAM: Malic enzyme	PF00390	243.6	258	572

			blastx.14	mitochondrial NAD(P)+ - dependent malic enzyme [Homo sapiens]	gi 187300 gb AAA36 197.1	99%	186	569
HMSHI83	1204709	217	blastx.2	malate dehydrogenase (NAD+) (EC 1.1.1.-) precursor, mitochondrial - human	pir A39503 A39503	98%	2	1720
HMSHI83	963083	770	HMMER 2.1.1	PFAM: Malic enzyme	PF00390	621.6	41	751
			blastx.14	mitochondrial NAD(P)+ - dependent malic enzyme [Homo sapiens]	gi 187300 gb AAA36 197.1	96% 72% 43%	2 753 855	784 785 902
HTEPM45	952389	218	HMMER 2.1.1	PFAM: Malic enzyme	PF00390	924.1	33	1175
			blastx.2	malate dehydrogenase (NAD+) (EC 1.1.1.-) precursor, mitochondrial - human	pir A39503 A39503	97%	33	1229
HTEPM45	953366	771	HMMER 2.1.1	PFAM: Fibrillar collagen C-terminal domain	PF01410	561.6	286	939
			blastx.2	prepro-alpha-1 type 3 collagen [Homo sapiens]	emb CAA32583.1	100% 59% 54% 54% 54% 53% 54% 48% 50%	37 31 37 37 31 37 37 43 43	942 126 132 129 129 126 129 129 126
HE8OV13	1228507	219	blastx.2	myosin heavy chain	pir S51823 S51823	44%	33	923

					ATM2 - Arabidopsis thaliana (fragment)		32%	1263	1484
HE8OV13	911341	772	HMMER 1.8		PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop)	PF00063	91.04	29	268
			blastx.14		myr 6 myosin heavy chain [Rattus norvegicus]	gi 1575333 gb AAB38840.1	46% 40% 40% 32%	41 617 608 449	274 742 697 559
HELGU27	1011928	220	blastx.2		MYOSIN I	sp Q63357 Q63357	93% 100%	1 788	786 817
HELGU27	923702	773	HMMER 2.1.1		PFAM: Myosin head (motor domain)	PF00063	256.3	8	640
			blastx.14		myosin I [Rattus norvegicus]	gi 3724141 emb CAA50871.1	97% 100% 100% 100%	11 688 662 719	640 717 676 736
HHEDC90	1226157	221	blastx.2		MYOSIN I	sp Q63357 Q63357	57%	216	3263
HHEDC90	911447	774	HMMER 2.1.1		PFAM: Myosin head (motor domain)	PF00063	241.2	25	597
			blastx.14		myosin I [Rattus norvegicus]	gi 3724141 emb CAA50871.1	67%	1	645
HNBRB59	685902	222	HMMER 1.8		PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop)	PF00063	94.31	85	243
			blastx.2		MYOSIN II NONMUSCLE (FRAGMENT)	sp Q91300 Q91300	92%	85	246
HNNBI16	965414	223	HMMER 2.1.1		PFAM: Myosin head (motor domain)	PF00063	116.7	101	292

HUJCL61	1223496	224	blastx.2	myosin I gamma, MMI gamma - mouse (fragment)	pir C45438 C45438	49%	101	337
			blastx.2	MYOSIN I	sp Q63357 Q63357	59% 47% 41%	159 2698 364	2717 3207 414
HUJCL61	911432	776	HMMER 2.1.1 blastx.14	PFAM: Myosin head (motor domain) myosin I [Rattus norvegicus]	PF00063 gi 3724141 emb CAA 50871.1	196	170	544
HWLRC68	1089187	225	blastx.2	Myosin X (Fragment).	sp AAF36524 AAF36 524	100% 92% 66%	90 1238 1267	1238 1276 1302
HWLRC68	911481	777	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	97.7	222	485
HFXFH42	713795	778	HMMER 1.8	PFAM: Neuraminidases	PF00064	9.26	259	354
HEQAN73	958912	227	HMMER 2.1.1 blastx.2	PFAM: Phosphoglycerate mutase family Hypothetical 30.1 kDa protein.	PF00300 sp CAC01127 CAC0 1127	64.2 99%	87 69	359 878
HSLFS31	1106294	228	blastx.2	right oriC-binding protein - Escherichia coli	pir JU0158 JU0158	99%	566	252
HSLFS31	921511	779	HMMER 2.1.1 blastx.14	PFAM: Phosphoglycerate mutase family Kenn Rudd identifies as gpmB [Escherichia coli]	PF00300 gi 537235 gb AAA97 291.1	71.6 96% 100%	12 3 188	149 188 223
HELGK56	1103702	229	blastx.2	pyruvate kinase (EC 2.7.1.40) A - Escherichia	pir S29790 S29790	96% 63%	572 619	96 554

HELGK56	925698	780	HMMER 2.1.1	coli PFAM: Pyruvate kinase	PF00224	406.9	147	731
			blastx.14	pyruvate kinase type II [Escherichia coli]	gi 147459 gb AAA24 473.1	98% 65%	147 21	731 107
HAMFW05	957586	230	HMMER 1.8	PFAM: Proyl oligopeptidase family	PF00326	33.83	1	174
			blastx.2	R26984.1 (FRAGMENT).	sp O75273 O75273	95%	1	558
HTEDG81	1193054	231	blastx.2	ALPHA 4 SUBUNIT OF 20S PROTEASOME.	sp Q9PTW9 Q9PTW 9	89%	79	771
HTEDG81	772995	781	HMMER 2.1.1	PFAM: Proteasome A- type and B-type	PF00227	114.6	180	488
HAMGO24	943287	232	HMMER 2.1.1	PFAM: Ribonucleotide reductases	PF00268	316.2	2	490
			blastx.2	hypothetical protein DKFZp761E1312.1 - human (fragment)	pir T46249 T46249	90%	2	550
HMWVBH91	1193044	233	blastx.2	house-keeping protein - mouse	pir S27870 S27870	53% 52%	282 121	1295 279
HMWVBH91	882083	782	HMMER 1.8	PFAM: Ribosomal RNA adenine dimethylases	PF00398	23.82	385	921
HOECH19	965639	234	HMMER 1.8	PFAM: Ribosomal RNA adenine dimethylases	PF00398	116.68	173	934
			blastx.2	CGI-75 PROTEIN.	sp Q9Y384 Q9Y384	95% 100% 100%	140 72 911	853 161 934
HSRAA80	1121919	235	blastx.2	POLYMERASE (FRAGMENT).	sp Q9UQG0 Q9UQG 0	63% 39%	17 421	361 498
HSRAA80	937640	783	HMMER	PFAM: Reverse	PF00078	20.88	11	130

			1.8	transcriptase (RNA-dependent DNA polymerase)					
			blastx.14	(AF080232) polymerase [Human endogenous retrovirus K]	gi 3600069 gb AAC63292.1	65%	17	325	
HHEDF50	1174682	236	blastx.2	nitrogen regulation protein II (EC 2.7.3.-) ntrB - Escherichia coli	pir A30377 RGECGL	89%	44	490	
HHEDF50	974396	784	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	115.35	65	490	
			blastx.14	NR(II) (glnL gene product) (AA 1-349) [Escherichia coli]	gi 41564 emb CAA28807.1	100%	86	427	
HHENK34	974395	237	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	62.83	56	277	
			blastx.2	nitrogen regulation protein II (EC 2.7.3.-) ntrB - Escherichia coli	pir A30377 RGECGL	78%	50	415	
HMAGK69	1105451	238	blastx.2	hypothetical 60.6 kD protein in deub-lysu intergenic region - Escherichia coli (strain K-12)	pir D65222 D65222	96% 100%	523 618	26 523	
HMAGK69	723186	785	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	40.87	31	405	
HNGNW52	1132300	239	blastx.2	protein-histidine kinase (EC 2.7.3.-) - Escherichia coli	pir G64840 G64840	93% 80% 90%	939 86 37	55 42 5	
HNGNW52	883074	786	HMMER	PFAM: Signal C terminal	PF00512	174.7	464	997	

			1.8	domain					
H6EDK67	974775	240	HMMER 2.1.1	PFAM: Signal peptidase I	PF00461	218.3	165	641	
			blastx.2	signal peptidase (EC 3.4.99.-) 21K chain - dog	pir A34229 A34229	98%	93	668	
HWBCS43	1151532	241	blastx.2	signal peptidase (EC 3.4.99.-) 18K chain - dog	pir A35309 A35309	93%	344	880	
HWBCS43	772564	787	HMMER 2.1.1	PFAM: Signal peptidase I	PF00461	117.2	381	653	
HCE3H71	961681	242	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	79.2	317	496	
			blastx.2	seizure-related protein SEZ-6 precursor - mouse	pir 52657 52657	83%	5	685	
						64%	565	957	
						30%	98	496	
						48%	929	1000	
HOFMS43	947973	243	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	64	174	302	
			blastx.2	PORCINE MEMBRANE COFACTOR PROTEIN.	sp O02839 O02839	47%	12	317	
HOVCO14	947999	244	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	84	21	170	
			blastx.2	UNKNOWN PROTEIN (FRAGMENT).	sp Q28797 Q28797	33%	21	347	
						34%	21	380	
						38%	424	516	
						47%	424	474	
HTOBE75	1161571	245	blastx.2	P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) 1-MOLECULE 3)	sp P16109 LEM3_H UMAN	95%	3	1067	
						38%	3	878	
						37%	3	866	
						35%	3	863	
						34%	3	866	

HTOBE75	591896	788	HMMER 2.1.1	(LECAM3). PFAM: Sushi domain (SCR repeat)	PF00084	39%	48	866
HCMSL08	898203	246	HMMER 2.1.1 blastx.2	PFAM: Calsequestrin	PF01216	1001.1	52	1221
HCMSL08	959176	789	HMMER 2.1.1 blastx.14	calsequestrin precursor, fast skeletal muscle - human	pir A60424 A60424	95%	112	1197
HDPBS64	846624	247	HMMER 1.8 blastx.2	calmitine; calsequestrine [Homo sapiens] PFAM: Thioredoxins	gi 688292 gb AAB32 063.1 PF00085	93% 116.87	1372 173	593 493
HDTBR50	846630	248	HMMER 1.8 blastx.2	ZK973.11 protein.	sp AAF40013 AAF40 013 PF00085	32%	182	652
HTDAB17	890384	249	HMMER 2.1.1 blastx.2	PFAM: Thioredoxins	PF00085	29.85	163	297
HABAE22	1227053	250	HMMER 2.1.1 blastx.2	NM23-H8. PFAM: Thioredoxin	sp AAF20909 AAF20 909 PF00085	100% 97% 107.9	130 327 276	327 467 533
HABAE22	965314	790	HMMER	CG1837 PROTEIN. CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN.	sp Q9VYV3 Q9VYV 3 sp Q9UNE7 Q9UNE7	42% 43% 41% 95%	225 231 348 169	518 539 533 1023
HABAE22	965314	790	HMMER	PFAM: TPR Domain	PF00515	38.4	300	383

			2.1.1 blastx.14	(AF039689) antigen NY-CO-7 [Homo sapiens]	gi 3170178 gb AAC18038.1	92%	171	725
HE9MI70	1217048	251	blastx.2	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 25 (EC 3.1.2.15) 1 PROTEASE 25)	sp P57080 UBPP_MOUSE	52%	15	758
HE9MI70	953319	791	HMMER 1.8	(DEUBIQUITINATING ENZYME 25).	PF00515	16.42	154	240
HHFDK15	854734	792	HMMER 2.1.1	PFAM: TPR Domain	PF00515	21.7	213	299
HOSNZ11	1162664	253	blastx.2	conserved hypothetical protein MTH68 - Methanobacterium 1	pir E69190 E69190	36%	134	448
HOSNZ11	965875	793	HMMER 2.1.1 blastx.14	PFAM: TPR Domain	PF00515	30.3	144	230
HTAEW05	1151514	254	blastx.2	(AE000798) O-linked GlcNAc transferase [Methanobacterium thermoautotrophicum]	gi 2621106 gb AAB84576.1	34% 23% 36%	249 3 395	362 236 484
HTAEW05	838562	794	HMMER 1.8	DJ979N1.1 (DJ979N1.1).	sp Q9UGR2 Q9UGR2	100%	215	658
HTTKN45	1181807	255	blastx.2	PFAM: TPR Domain	PF00515	16.51	460	546
				BCDNA:GH04929 PROTEIN.	sp Q9V3G6 Q9V3G6	23%	420	1583

HTTKN45	914589	795	HMMER 1.8 blastx.14	PFAM: TPR Domain (AF181631) BcDNA.GH04929 [Drosophila melanogaster]	PF00515	18.74	383	469
HUSJN62	923146	256	HMMER 2.1.1 blastx.2	PFAM: TPR Domain CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN.	gi 5901818 gb AAD5 5417.1 AF181631_1 PF00515	46% 26% 38.4	539 386 1075	685 487 992
HTEIU92	1102681	257	blastx.2	Transketolase (EC 2.2.1.1).	sp AAF76194 AAF76 194	71%	1	564
HTEIU92	870652	796	HMMER 2.1.1 blastx.2	PFAM: Transketolase	PF00456	70.1	1	225
HAQMD86	1105267	258	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 10 (EC 3.1.2.15) 1 1	sp Q14694 UBPA_H UMAN	96%	13	1878
HAQMD86	961459	797	HMMER 2.1.1 blastx.14	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 similar to ubiquitin- specific proteinase of S.cerevisiae. [Homo sapiens]	PF00443 gi 136438 dbj BAA1 1507.1	89.1 96%	1700 2	1900 1879
HBJJG02	1151462	259	blastx.2	CG5794 PROTEIN.	sp Q9VC56 Q9VC56	48%	795	1409
HBJJG02	919508	798	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal	PF00443	80.6	176	460

HBJN65	1151463	260	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 25 (EC 3.1.2.15) 1 PROTEASE 25) (DEUBIQUITINATING ENZYME 25).	sp P57080 UBPP_M OUSE	56% 26% 55% 25% 25% 46% 31% 22%	164 314 50 485 626 281 821 188	253 481 103 613 709 319 886 268
HBJN65	960507	799	HMMER 2.1.1 blastx.14	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 similar to ubiquitin carboxyl-terminal hydrolase; 1 1 cDNA EST EMBL:D64405 comes from this gene; cDNA EST EMBL:D68146	PF00443 gj 3878110 emb CAA 87786.1	80.5 40% 40%	514 409 607	723 588 681
HBMUJ35	1195500	261	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 23 (EC	sp Q9UK80 UBPN_H UMAN	91%	1982	288

HBMUJ35	956041	800	HMMER 2.1.1 blastx.14	3.1.2.15)11 PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 (AF177758) ubiquitin specific protease 16 [Homo sapiens]	PF00443	54.6	492	355
HCEBP60	1227635	262	blastx.2	LSFR3 PROTEIN (FRAGMENT).	sp Q9W6U5 Q9W6U 5	85% 75%	1737 2863	2846 2910
HCEBP60	812297	801	HMMER 1.8	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00443	59.49	168	281
HFGMA55	1150870	263	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 23 (EC 3.1.2.15)11	sp Q9UK80 UBPN_H UMAN	100%	10	444
HFGMA55	858681	802	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	57.8	237	377
HLHTE91	789603	264	HMMER 2.1.1 blastx.2	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 DEUBIQUITINATING ENZYME.	PF00443 sp Q9UNP0 Q9UNP0	92.4 40%	862 409	1068 1077
HLHTE91	868803	803	HMMER 2.1.1	PFAM: MYND finger	PF01753	33.7	393	521
HLYFI58	1151495	265	blastx.2	UBIQUITIN CARBOXYL- TERMINAL	sp Q9Y5T5 UBPG_H UMAN	100%	2	625

					HYDROLASE 16 (EC 3.1.2.15) 1 1 1					
HLFYI58	924193	805	HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	77.4	368	619	
			blastx.14		(AF126736) ubiquitin processing protease [Homo sapiens]	gi 4454565 gb AAD20949.1	100%	2	625	
HNNBJ44	915273	806	HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	50.1	1045	1131	
			blastx.14		similar to ubiquitin carboxyl-terminal hydrolase; 1 1 cDNA EST EMBL:D34547 comes from this gene; cDNA EST EMBL:D37684	gi 3879501 emb CAA87795.1	44% 28% 42% 35% 23% 72%	688 292 1276 1093 1961 1057	915 462 1332 1134 2062 1089	
HSLJI46	997643	267	blastx.2		UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) 1 1	sp P40818 UBP8_HUMAN	82% 100% 79%	64 1 510	498 87 596	
HSLJI46	883028	807	HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	99.8	1336	1521	
HTFOK70	1151518	268	blastx.2		CG3016 PROTEIN.	sp Q9W462 Q9W462	56% 41% 63.6	361 16 359	561 153 568	
HTFOK70	914561	808	HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443				

			blastx.14	(AC003974) putative ubiquitin specific protease [Arabidopsis thaliana]	gi 2914695 gb AAC0 4485.1	60%	473	571
HUSXO71	1164014	269	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 18 (EC 3.1.2.15) 1 1 1	sp Q9UMW8 UBPI_ HUMAN	39% 37%	7 368	129 472
HUSXO71	862649	809	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	65.2	1290	1505
HWBDP39	1223498	270	blastx.2	CDNA FLJ20314 FIS, CLONE HEP07831.	sp BAA91084 BAA9 1084	88%	1313	2239
HWBDP39	810403	810	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	55.2	227	382
HKMMQ73	840459	271	HMMER 1.8	PFAM: UDP- glucuronosyl and UDP- glucosyl transferases	PF00201	93.48	28	327
			blastx.2	2-hydroxyacylsphingosine 1-beta- galactosyltransferase (EC 1	pir JC5423 JC5423	88%	7	417
HVVVK72	1179755	272	blastx.2	glucuronosyltransferase (EC 2.4.1.17) UGT2B13 precursor - rabbit	pir B47113 B47113	35%	69	461
HVVVK72	933167	812	HMMER 1.8	PFAM: UDP- glucuronosyl and UDP- glucosyl transferases	PF00201	70.01	2	391
H7TXB52	981972	273	blastx.2	DUAL SPECIFICITY	sp Q9UNI6 DUSC_H	100%	303	1322

				PROTEIN PHOSPHATASE 12 (EC 3.1.3.48) (EC 1	UMAN			
H7TXB52	910910	813	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	117.9	378	806
			blastx.14	(AB004537) PROTEIN- TYROSINE PHOSPHATASE YVH1 [Schizosaccharomyces pombe]	gi 2257526 dbj BAA2 1420.1	26% 48% 52% 38%	516 1143 1092 960	968 1292 1142 1013
HDPY71	1217205	274	blastx.2	Mitogen-activated protein kinase phosphatase x.	sp AAF86649 AAF86 649	99% 100%	531 392	848 529
HDPY71	971345	814	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	109.1	492	719
			blastx.14	DsPTP1 protein [Arabidopsis thaliana]	gi 4150963 emb CAA 77232.1	48% 43%	492 377	716 487
HGOCA12	968763	275	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	28.6	112	360
			blastx.2	PROTEIN PHOSPHATASE.	sp Q9UII6 Q9UII6	40%	25	360
HGOCA12	971583	815	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	60.1	467	318
			blastx.14	phosphatase tyrosine/serine [Homo sapiens]	gi 181840 gb AAA35 777.1	48%	515	318
HHCJ29	1077517	276	blastx.2	hypothetical protein	pir T14756 T14756	100%	490	1716

[illegible]

HMIAO23	675329	819	HMMER 2.1.1	INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.	PF00043	29.5	23	184
HELDW45	944301	282	HMMER 2.1.1	PFAM: Glutathione S- transferases.	PF00408	133.1	114	512
			blastx.2	Phosphoglucosyltransferase/phosphomannomutase	pir G64803 G64803	99%	3	512
HSRBB31	1121889	283	blastx.2	phosphoglucosyltransferase (EC 5.4.2.2) - Escherichia coli	sp BAA99407 BAA9 9407	100% 64% 54% 71%	3 493 395 707	440 861 526 790
HSRBB31	958210	820	HMMER 1.8	3-methylcrotonyl-CoA carboxylase biotin- containing 1	PF00364	75.97	1455	1643
HTEOW39	1151517	284	blastx.2	PFAM: Biotin-requiring enzymes	pir JE0185 JE0185	49%	65	484
HTEOW39	870566	821	HMMER 1.8	lysozyme (EC 3.2.1.17) - bare-faced crassow	PF00062	126.92	59	295
HE2PE32	1106571	285	blastx.2	PFAM: C-type lysozymes and alpha-lactalbumin	pir B65175 B65175	85%	1	540
HE2PE32	524511	822	HMMER 1.8	6-phospho-beta- glucosidase (EC 3.2.1.86) bg B - Escherichia coli	PF00232	87.26	17	289
HSIDW39	1211446	286	blastx.2	PFAM: Glycosyl hydrolases family 1	sp CAC08178 CAC0 8178	99%	56	748
HSIDW39	775139	823	HMMER 2.1.1	Cytosolic beta- glucosidase (Fragment).	PF00232	134	28	372

				blastx.2	cytosolic beta-glucosidase [Cavia porcellus]	gb AAB41058.1	84%	1	363
HSIDW39	830774	824		HMMER 2.1.1	PFAM: Glycosyl hydrolase family 1	PF00232	155.5	42	419
HPMLD30	1226192	287		blastx.2	alpha-glucosidase (EC 3.2.1.20) - Escherichia coli	pir C64769 C64769	96%	44	1543
HPMLD30	937414	825		HMMER 1.8	PFAM: Alpha amylases (family of glycosyl hydrolases)	PF00128	18.21	402	479
				blastx.2	maltodextrin glucosidase [Escherichia coli]	gb AAB40159.1	99%	30	485
HOEKP17	1204712	288		blastx.2	FLAVOHEMOPROTEIN B5+B5R.	sp Q9UHI9 Q9UHI9	90% 97%	749 214	1675 870
HOEKP17	931049	826		HMMER 2.1.1	PFAM: Heme-binding domain in cytochrome b5 and oxidoreductases	PF00173	69.6	258	428
				blastx.14	(AL032654) similar to Heme-binding domain in 1	gi 3881161 emb CAA 21721.1	60% 35% 36% 60% 50% 39% 57% 55% 45%	261 1118 906 156 1253 1565 1352 1055 580	473 1285 1013 215 1318 1648 1393 1081 639
HFXDP67	1228141	289		blastx.2	hypothetical protein b0872 - Escherichia coli	pir H64825 H64825	95%	240	1205
HFXDP67	526951	827		HMMER 1.8	PFAM: FAD/NAD- binding domain in	PF00175	13.6	293	415

HJABA59	1199933	290	blastx.2	oxidoreductases	sp Q9UBK8 Q9UBK8	91%	2	904
HJABA59	713642	828	HMMER 1.8	PFAM: FAD/NAD-binding domain in oxidoreductases	PF00175	100.6	423	797
HKIXB03	1129055	291	blastx.2	CYTOCHROME B5 REDUCTASE B5R.2.	sp Q9UHI0 Q9UHI0	93% 82% 88%	197 2 70	370 88 96
HKIXB03	924636	829	HMMER 1.8	PFAM: FAD/NAD-binding domain in oxidoreductases	PF00175	31.48	192	326
			blastx.2	(AL133582) hypothetical protein [Homo sapiens]	emb CAB63726.1	85%	144	371
HKMMF49	1124742	292	blastx.2	Kidney superoxide-producing NADPH oxidase.	sp BAA95695 BAA95695	100%	10	600
HKMMF49	677960	830	HMMER 2.1.1	PFAM: Ferric reductase like transmembrane component	PF01794	63.6	79	294
HLD0G51	1151491	293	blastx.2	Neurospora crassa hypothetical protein 15E6.170 - Neurospora crassa	pir T48809 T48809	40% 32%	163 654	522 800
HLD0G51	918840	831	HMMER 2.1.1	PFAM: Oxidoreductase FAD/NAD-binding domain	PF00175	62.6	524	904
			blastx.14	phenolhydroxylase component [Acinetobacter	gi 535285 emb CAA85385.1	32% 36%	269 860	370 967

HSVAI25	1130819	294	blastx.2	calcoaceticus]		sp BAB12124 BAB12124	37%	647	727
HSVAI25	577154	832	HMMER 1.8	Hypothetical 12.9 kDa protein.		PF00175	42%	527	583
HSXCP56	924635	295	HMMER 2.1.1	PFAM: FAD/NAD-binding domain in oxidoreductases			44%	215	268
HBCAT08	1167275	296	blastx.2	CYTOCHROME B5 REDUCTASE B5R.2.		sp Q9UHHJ Q9UHHJ0	58%	524	652
HBCAT08	920940	833	HMMER 1.8	PXN PROTEIN.		sp Q9VZZ4 Q9VZZ4	66%	663	761
HBFBU53	1048855	297	blastx.2	PFAM: Peroxidases		PF00141	7.34	126	212
HBFBU53	837647	834	HMMER 2.1.1	similar to D.melanogaster peroxidase(U11052) [Homo sapiens]		gi 1504040 dbj BAA13219.1	162.3	243	500
HTTDO45	942505	298	HMMER	subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - human		pir A39490 A39490	91%	171	950
				PFAM: Proprotein convertase P-domain		PF01483	100%	142	240
				PFAM: Thiolase		PF00108	49%	71	2419
							37%	2237	2461
							50%	3295	3351
							36%	157	246
							32.87	3	347
							92%	183	347
							93%	3	134
							92%	160	198
							29%	133	183
							85%	4	570
							254.1	381	797
							794.8	459	1637

			2.1.1		3-oxoacyl-CoA thiolase - human	pir S43440 S43440			456	1640
			blastx.2					92%		
HTPII72	1104236	299	blastx.2		valine--tRNA ligase (EC 6.1.1.9) - rat (fragment)	pir PN0473 PN0473		51%	4	657
HTPII72	958035	835	HMMER 1.8		PFAM: tRNA synthetases class I	PF00133		280.02	4	645
			blastx.14		transfer RNA-Val synthetase [Rattus norvegicus]	gi 207625 gb AAA42320.1		56% 51% 58%	4 589 780	576 750 866
H6BSE22	1151371	300	blastx.2		UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (EC 3.1.2.15) 1 1 1	sp Q9Y5T5 UBPG_HUMAN		99%	156	623
H6BSE22	969019	836	HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442		41.8	738	833
			blastx.14		(AF126736) ubiquitin processing protease [Homo sapiens]	gi 4454565 gb AAD20949.1		94% 100% 94% 100% 42% 50%	672 156 1482 1573 1452 781	1493 602 1538 1599 1514 810
HDPAB43	1220621	301	blastx.2		Ubiquitin specific protease (Fragment).	sp AAF66953 AAF66953		80%	114	1586
HDPAB43	864998	837	HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442		63.9	236	331
HDPFM16	1193042	302	blastx.2		CG8830 PROTEIN.	sp Q9V6C0 Q9V6C0		53%	180	470

HDPFM16	810401	838	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	50% 30% 41% 41%	983 1571 611 1319	1201 1828 778 1435
HFPCN10	1151478	303	blastx.2	CDNA FLJ10809 FIS, CLONE NT2RP4000927, WEAKLY SIMILAR TO 1.1	sp BAA91825 BAA9 1825	62% 69%	163 330	258 518
HFPCN10	915568	839	HMMER 1.8 blastx.14	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	PF00442 gi 3560166 emb CAA 20678.1	32.31% 50% 33%	417 345 466	470 464 555
HLQFO35	933901	840	HMMER 1.8	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	11.44%	131	181
HMWIU94	1150834	305	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 12 (EC 3.1.2.15) 1.1.1	sp O75317 UBPC_H UMAN	92%	162	536
HMWIU94	705880	841	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	58.8%	231	326

HSATQ28	1124600	306	blastx.2	PRO0758.	sp AAF71030 AAF71030	86%	222	491
HSATQ28	866951	842	HMMER 1.8	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	11.1	90	122
HTPIL46	1196787	307	blastx.2	Cyld protein.	sp CAB93333 CAB93333	99%	963	1859
						99%	246	962
						99%	1870	2265
						37%	669	842
						37%	1596	1754
HTPIL46	973570	843	HMMER 2.1.1	PFAM: CAP-Gly domain	PF01302	28.2	872	955
			blastx.2	(AF161542) HSPC057 [Homo sapiens]	gb AAF29029.1 AF161542_1	93%	626	2167
						100%	2143	2169
						45%	512	577
HNGEN37	1103305	308	blastx.2	indole-3-glycerol-phosphate synthase (EC 4.1.1.48) / 1 coli	pir A64874 GWEC	99%	1	531
HNGEN37	663955	844	HMMER 2.1.1	PFAM: Indole-3-glycerol phosphate synthases	PF00218	125.4	2	223
HLMDO77	974855	309	HMMER 1.8	PFAM: Trypsin	PF00089	114.97	116	523
			blastx.2	Complement C1r-like proteinase precursor.	sp AAF44349 AAF44349	100%	116	547
HNKAZ51	1154961	310	blastx.2	SERINE PROTEASE DESC1.	sp Q9UL52 Q9UL52	48%	100	957
HNKAZ51	947067	846	HMMER 1.8	PFAM: Trypsin	PF00089	124.58	259	594
			blastx.2	(AF064819) serine protease DESC1 [Homo	gb AAF04328.1 AF064819_1	42%	100	603
						35%	677	832

HOGDR01	919899	311	HMMER 1.8	sapiens] PFAM: Trypsin	PF00089	46%	603	686
HOGDR01	947085	847	blastx.2 HMMER 1.8	SP001LA (FRAGMENT). PFAM: Trypsin	sp O43342 O43342 PF00089	322.84	171	881
			blastx.2	(AC003965) SP001LA [Homo sapiens]	gb AAB93671.1	99%	165	890
HUKEP18	957456	312	HMMER 1.8	PFAM: Trypsin	PF00089	320.16	161	871
			blastx.2	TESTES-SPECIFIC PROTEIN TSP50.	sp Q9UJ38 Q9UJ38	99%	155	967
HWHGF95	1155021	313	blastx.2	KALLIKREIN 9 PRECURSOR (EC 3.4.21.-) (KALLIKREIN- LIKE 1	sp Q9UKQ9 KLK9_ HUMAN	100%	735	340
			HMMER 1.8	PFAM: Trypsin	PF00089	94%	36	743
HWHGF95	947019	848	blastx.2	(AF135026) kallikrein- like protein 3 KLK-L3 [Homo sapiens]	gb AAD26427.2 AF1 35026_1	309.92	56	724
			HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	93%	35	742
HEMFC61	836514	314	blastx.2	RETINALDEHYDE- SPECIFIC DEHYDROGENASE TYPE 2 (EC 1.2.1.-) (RALDH(II)) (RALDH- 2).	sp O94788 DHAS_H UMAN	397.1	10	642
						98%	4	642
HEOQP44	942596	315	HMMER	PFAM: Beta-lactamase	PF00144	420.7	250	1026

				2.1.1 blastx.2	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	95%	169	1026
HHEKZ12	878267	316		HMMER 1.8	PFAM: Beta-lactamases	PF00144	132.1	102	380
				blastx.2	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	98% 65%	21 377	377 436
HHELA35	878217	317		HMMER 2.1.1	PFAM: Beta-lactamase	PF00144	175.4	118	450
				blastx.2	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	98%	37	450
HSYBQ34	972295	849		HMMER 1.8	PFAM: Beta-lactamases	PF00144	387.58	2697	3473
HFCBA44	948533	319		HMMER 1.8	PFAM: Carboxylesterases	PF00135	34.24	315	485
				blastx.2	thiolesterase B (EC 3.-.-.-) precursor - mallard	pir A47162 A47162	56% 60% 48%	2 423 184	208 482 264
HOUBE50	948519	320		HMMER 1.8	PFAM: Carboxylesterases	PF00135	55.97	16	243
				blastx.2	Neurologin 3 isoform HNL3s (Fragment).	sp AAF71231 AAF71 231	70%	31	243
HDPAS16	734057	321		HMMER 2.1.1	PFAM: Carbamoyl- phosphate synthase (CPSase)	PF00289	137.8	220	495
				blastx.2	3-methylcrotonyl-CoA carboxylase biotin- containing 1	sp BAA99407 BAA9 9407	89%	112	495
HFLAA23	960332	322		HMMER 2.1.1	PFAM: FGYY family of carbohydrate kinases	PF00370	314	137	784

				blastx.2	L-xylulokinase (EC 2.7.1.53) - Escherichia coli	pir[S47801]S47801	86%	8	784
HCFMZ90	922112	323	HMMER 1.8		PFAM: Beta-ketoacyl synthases	PF00109	194.57	291	872
			blastx.2		CDNA FLJ20604 FIS, CLONE KAT06449.	sp BAA91286 BAA91286	92% 98% 59%	255 67 5	866 300 100
HFCE27	1103330	324	blastx.2		CDNA FLJ20604 FIS, CLONE KAT06449.	sp BAA91286 BAA91286	94% 86%	506 198	1120 491
HFCE27	922115	850	HMMER 2.1.1		PFAM: Beta-ketoacyl synthase	PF00109	206.2	372	1001
			blastx.14		(AE000752) 3-oxoacyl-[acyl-carrier-protein] synthase II [Aquifex aeolicus]	gi 2984031 gb AAC07574.1	53% 78% 75% 37%	393 195 939 250	920 251 986 297
HSDFK78	1155464	325	blastx.2		biotin sulfoxide reductase (EC 1.-.-.-) 2 - Escherichia coli	pir H64949 H64949	89%	1	306
HSDFK78	582754	851	HMMER 2.1.1		PFAM: Prokaryotic molybdopterin oxidoreductases	PF00384	34.8	297	374
HSDJX58	891067	326	HMMER 1.8		PFAM: NADH-Ubiquinone/plastoquinone, various chains	PF00361	97.09	1128	1487
			blastx.2		hypothetical protein b2484 - Escherichia coli (strain K-12)	pir C65024 C65024	82%	735	1487
HSDJX58	956591	852	HMMER 1.8		PFAM: NADH-Ubiquinone/plastoquinone	PF00361	100.08	387	19

				, various chains				
			blastx.2	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 [Escherichia coli]	dbj BAA16372.1	100%	814	1572
HSLHV27	1105339	327	blastx.2	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain L - Escherichia coli	pir D64999 D64999	93%	94	927
HSLHV27	964075	853	HMMER 2.1.1	PFAM: NADH-Ubiquinone/plastoquinone (complex I), various chains	PF00361	115.1	917	615
			blastx.2	NADH dehydrogenase I, submit nuol [Escherichia coli]	emb CAA48371.1	99%	91	954
HNGFU12	1128272	328	blastx.2	REVERSE TRANSCRIPTASE (476 AA) (FRAGMENT).	sp Q85732 Q85732	55%	109	543
HNGFU12	971170	854	HMMER 1.8	PFAM: RNase H	PF00075	55.68	102	290
			blastx.14	reverse transcriptase (476 AA) [Woolly monkey sarcoma virus]	gi 930259 emb CAA33367.1	44% 60%	96 1	422 75
HWLKA89	1105515	329	blastx.2	POL.PROTEIN.	sp Q9WTK9 Q9WTK9	51% 54% 55% 64%	560 885 135 448	186 577 1 398
HWLKA89	735158	855	HMMER 1.8	PFAM: RNase H	PF00075	47.76	25	165
HLWRU48	1162653	330	blastx.2	ENDOGENOUS	sp O15803 O15803	84%	739	984

HLWBU48	721520	856			RETROVIRUS HERV-K(HML6) PROVIRAL CLONE HML6.17.1.1				77%	672	752
				HMMER 1.8	PFAM: Retroviral aspartyl proteases						
HWWEY71	1204720	331		blastx.2	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR 1		sp P34897 GLYM_H_UMAN		97% 97%	595 113	1623 619
HWWEY71	970546	857		HMMER 2.1.1 blastx.14	PFAM: Serine hydroxymethyltransferase SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR 1 (SHMT)		PF00464 sp P34897 GLYM_H_UMAN		423.3 90%	257 113	763 859
HHFGD45	1151161	332		blastx.2	superoxide dismutase (EC 1.15.1.1) (Mn) sodA [validated] - Escherichia coli		pir A24141 DSECN		100%	880	290
HHFGD45	584855	858		HMMER 1.8	PFAM: Iron/manganese superoxide dismutases (SODM)		PF00081		111.46	133	267
HNHEB44	1161293	333		blastx.2	superoxide dismutase (EC 1.15.1.1) (Mn) sodA [validated] - Escherichia coli		pir A24141 DSECN		100%	23	613
HNHEB44	683284	859		HMMER 1.8	PFAM: Iron/manganese superoxide dismutases		PF00081		100.87	31	150

HMACX92	1151497	334	blastx.2	(SODM) L-serine dehydratase (EC 4.2.1.13) - rat	pir S01009 DWRRTT	50%	176	1132
HMACX92	922250	860	HMMER 2.1.1	PFAM: Pyridoxal-phosphate dependent enzyme	PF00291	224.5	203	1105
			blastx.2	serine dehydratase (AA 1 - 327) [Rattus norvegicus]	emb CAA68721.1	61%	197	1153
HNTBW57	1193070	335	blastx.2	CDNA FLJ10916 FIS, CLONE OVARC1000309, WEAKLY SIMILAR TO 1	sp BAA91904 BAA91904	80% 100%	958 613	1302 777
HNTBW57	867327	861	HMMER 1.8	PFAM: Serine/threonine dehydratases, cysteine synthase and cystathionine	PF00291	41.43	425	673
HBSDC13	1105677	336	blastx.2	tartronate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli	pir JT0742 JT0742	68% 83% 51% 85% 96%	353 124 622 840 47	718 423 990 959 130
HBSDC13	657402	862	HMMER 1.8	PFAM: Thiamine pyrophosphate enzymes	PF00205	26.75	3	182
HCWBX21	920486	337	HMMER 1.8	PFAM: Thiamine pyrophosphate enzymes	PF00205	22.15	82	261
			blastx.2	tartronate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli	pir JT0742 JT0742	88% 96% 43%	85 8 374	369 91 442
HFRBW72	916944	338	HMMER 2.1.1	PFAM: Thiamine pyrophosphate enzymes	PF00205	92.9	443	664

			blastx.2	pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli	pir A23648 DEECPC	81%	407	676
HSLJX23	1105530	339	blastx.2	tartarate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli	pir JT0742 JT0742	98%	2	496
HSLJX23	837470	863	HMMER 1.8	PFAM: Thiamine pyrophosphate enzymes	PF00205	57.57	2	193
HSLJX90	1105297	340	blastx.2	pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli	pir A23648 DEECPC	100%	1	438
HSLJX90	787575	864	HMMER 2.1.1	PFAM: Thiamine pyrophosphate enzymes	PF00205	95.2	2	274
HAUAI67	1102604	341	blastx.2	HSPC150.	sp AAF29114 AAF29 114	100%	137	727
HAUAI67	929241	865	HMMER 1.8	PFAM: Ubiquitin- conjugating enzymes	PF00179	128.71	236	508
			blastx.14	ubiquitin-conjugating enzyme [Schizosaccharomyces pombe]	gi 2330662 emb CAB 11183.1	54% 67% 32%	344 242 132	514 334 224
HDPTA89	953718	342	HMMER 1.8	PFAM: Ubiquitin- conjugating enzymes	PF00179	74.19	173	424
			blastx.2	UBC6P HOMOLOG.	sp Q9QX58 Q9QX58	95%	173	430
HMCBN45	927125	343	HMMER 1.8	PFAM: Ubiquitin- conjugating enzymes	PF00179	115.78	234	677
			blastx.2	hypothetical protein R09B3.4 - Caenorhabditis elegans	pir T24069 T24069	53%	216	680
HTTJY18	1223495	344	blastx.2	Non-Canonical Ubiquitin	sp CAB83212 CAB8	83%	376	1281

					Conjugating Enzyme 1 (NCUBE1).	3212	100%	330	365
HTTJY18	950989	866	HMMER 1.8		PFAM: Ubiquitin- conjugating enzymes (AF151834) CGI-76 protein [Homo sapiens]	PF00179	73.94	334	657
HMAJL09	1157337	345	blastx.2		hypothetical 29.7K protein, ibpA-gyrB intergenic region - Escherichia coli (strain K- 12)	gb AAD34071.1 AF1 51834.1 pir B65172 QQECGB	99% 98%	292 269	1263 526
HMAJL09	950168	867	HMMER 1.8		PFAM: ADP-glucose pyrophosphorylase	PF00483	150.92	20	256
HSVCH37	558195	346	blastx.14		f270 [Escherichia coli]	gi 290545 gb AAA62 048.1	100% 100%	254 468	469 512
HTOCG37	708888	347	HMMER 2.1.1		PFAM: 3'5'-cyclic nucleotide phosphodiesterase	PF00233	30	18	98
HBXAW47	771624	348	HMMER 2.1.1		PFAM: 3'5'-cyclic nucleotide phosphodiesterase	PF00233	65.1	42	215
HBXAW27	909801	349	blastx.2		3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 8B, 1	pir JE0293 JE0293	100% 53%	6 179	203 340
			HMMER 2.1.1		PFAM: Protein phosphatase 2C	PF00481	80.5	273	560
			blastx.2		PROTEIN PHOSPHATASE 2C.	sp Q9Z1Z6 Q9Z1Z6	85%	270	578
			HMMER 2.1.1		PFAM: Phosphatidylinositol-	PF00388	113.6	1642	1797

				specific phospholipase C, X domain					
			blastx.2	Phospholipase C-beta-1a.	sp CAB98142 CAB98142	97%	1243	1803	
HSLJE54	926924	350	HMMER 2.1.1	PFAM: Pyridoxal-dependent decarboxylase conserved domain	PF00282	35.8	342	536	
			blastx.2	CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 4.	sp Q9UNJ5 Q9UNJ5	98% 92% 85% 100%	198 542 721 885	548 739 885 908	
HBXBG65	932780	351	HMMER 1.8	PFAM: Cytochrome P450	PF00067	46.55	2	535	
			blastx.2	CHOLESTEROL 24-HYDROXYLASE.	sp Q9Y6A2 Q9Y6A2	98%	2	535	
HB8CG83	933609	352	HMMER 2.1.1	PFAM: Protein phosphatase 2C	PF00481	42.6	757	942	
			blastx.2	SCOP.	sp Q9WTR8 Q9WTR8	90% 70% 70% 60% 43% 30% 36%	321 712 1 977 41 118 369	707 1110 348 1021 151 279 443	
HOGCW55	953161	353	HMMER 2.1.1	PFAM: Aminotransferases class-V	PF00266	56.5	132	341	
			blastx.2	probable phosphoserine transaminase (EC 2.6.1.52), progesterone-	pir A26998 A26998	85% 77%	132 355	356 381	

HNTND64	954871	354	HMMER 2.1.1 blastx.2	induced, endometrial - rabbit PFAM: Cytochrome P450	PF00067	28.2	10	225
				cytochrome P450 - golden hamster	pir 48164 48164	37% 47%	10 261	264 329
HHAWC08	957942	355	HMMER 1.8	PFAM: IMP dehydrogenase / GMP reductase	PF00478	231.99	361	978
			blastx.2	Guanosine monophosphate reductase isolog.	sp BAA93080 BAA9 3080	100% 100%	334 975	975 1376
HFPEN04	964824	356	HMMER 1.8 blastx.2	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	33.54	259	489
				CG8745 PROTEIN.	sp Q9VU95 Q9VU95	62%	148	492
HTZMB51	496523	357	HMMER 2.1.1 blastx.2	PFAM: Lyase adenylosuccinate lyase (EC 4.3.2.2) - Escherichia coli	PF00206 pir S19212 S19212	112.9 97% 71%	61 73 2	399 399 127
HNHDK43	529500	358	HMMER 1.8 blastx.2	PFAM: tRNA synthetases class II lysine--tRNA ligase (EC 6.1.1.6) - Escherichia coli	PF00152 pir B65073 SYECKT	55.51 85% 90%	208 58 368	372 372 397
HTTDP32	558751	359	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (L, M and V) PROBABLE LEUCYL- TRNA SYNTHETASE, MITOCHONDRIAL	PF00133 sp Q15031 SYLM_H UMAN	76 98% 84% 45%	7 1 267 320	261 261 365 424

HSLEP27	572920	360	HMMER 2.1.1 blastx.2	PRECURSORS 1 PFAM: tRNA synthetases class I (I, L, M and V) leucine-tRNA ligase (EC 6.1.1.4) [validated] - Escherichia coli	PF00133 pir H64798 SYECL	133.5 96% 96%	5 14 405	409 599
HMTAL73	621705	361	HMMER 2.1.1 blastx.2	PFAM: Isocitrate and isopropylmalate dehydrogenases isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) beta chain isoform B - human	PF00180 pir T13147 T13147	94.5 75% 100%	241 103 2	423 450 100
HMHQBQ53	715301	362	HMMER 2.1.1 blastx.2	PFAM: Nucleotidyl transferase GDP-MANNOSE PYROPHOSPHORYLAS E A.	PF00483 sp Q9Y5P5 Q9Y5P5	45.8 100% 100%	237 231 376	368 377 423
HBICG44	715860	363	HMMER 2.1.1 blastx.2	PFAM: Thiolase 3-oxoacyl-CoA thiolase - human	PF00108 pir S43440 S43440	33.1 100%	189 189	272 272
HSKXN70	753717	364	HMMER 2.1.1 blastx.2	PFAM: TPR Domain CG5038 PROTEIN. PFAM: Histidine acid phosphatase acid phosphatase (EC 3.1.3.2) precursor - Escherichia coli	PF00515 sp Q9VF81 Q9VF81 PF00328 pir B36733 B36733	31.4 40% 118.4 77% 92%	267 114 75 3 341	347 344 338 518 463

HFFP57	835955	366	HMMER 2.1.1	PFAM: Signal peptidase I	PF00461	32.1	218	514
HFKJW01	836491	367	blastx.2	CG11110 PROTEIN.	sp Q9V959 Q9V959	57%	140	574
			HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	174	96	440
			blastx.2	lactaldehyde dehydrogenase (EC 1.2.1.22) aldA - Escherichia coli	pir A38165 A38165	100%	96	440
HSDFL63	836498	368	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	127.4	1	234
			blastx.2	RETINALDEHYDE- SPECIFIC DEHYDROGENASE TYPE 2 (EC 1.2.1.-) (RALDH(II)) (RALDH- 2).	sp Q94788 DHAS_H UMAN	100%	1	249
HLD0008	857070	369	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	32.4	36	137
			blastx.2	CDNA FLJ10785 FIS, CLONE NT2RP4000457, WEAKLY SIMILAR TO 1	sp BAA91807 BAA9 1807	100% 80%	3 403	401 570
HMSHN43	867363	370	HMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	53.7	70	231
			blastx.2	GDP-MANNOSE PYROPHOSPHORYLAS E A.	sp Q9Y5P5 Q9Y5P5	90%	64	342
HBXCT92	871044	371	HMMER	PFAM: Nucleotidyl	PF00483	49.7	105	473

				transferase						
				blastx.2 HMMER	Eukaryotic translation initiation factor EIF2B subunit 3.	sp AAAF91351 AAF91351	97%	96	1451	
H6EDP44	875744	372		2.1.1 HMMER	PfAM: Nucleotidyl transferase	PF00483	129.6	190	768	
				blastx.2 HMMER	GDP-MANNOSE PYROPHOSPHORYLAS E B.	sp Q9Y5P6 Q9Y5P6	99% 100% 100% 32%	199 804 65 837	801 968 187 938	
HLJBF94	875745	373		2.1.1 HMMER	PfAM: Nucleotidyl transferase	PF00483	89.2	261	539	
				blastx.2 HMMER	GDP-MANNOSE PYROPHOSPHORYLAS E B.	sp Q9Y5P6 Q9Y5P6	81%	258	668	
HTEHO28	877182	374		1.8 HMMER	PfAM: Pyridine nucleotide-disulphide oxidoreductases class-I	PF00070	206.97	1166	441	
				blastx.2 HMMER	Thioredoxin reductase TR2 (Fragment).	sp AAD51325 AADS1325	97% 85% 97% 41%	1226 1857 2123 1383	432 1147 1869 1315	
HE9PC30	880696	375		1.8 HMMER	PfAM: Ubiquitin-conjugating enzymes CGI-76 PROTEIN.	PF00179	69.1	85	285	
				blastx.2 HMMER		sp Q9Y385 Q9Y385	98% 96% 60%	43 555 527	381 638 586	
HILMDN29	881288	376		2.1.1 HMMER	PfAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	34.2	315	506	

			blastx.2	CG8830 PROTEIN.	sp Q9V6C0 Q9V6C0	43%	9	218
HWBCF78	911355	377	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	31%	399	503
			blastx.2	myosin-1f - mouse	pir A59300 A59300	89%	148	288
HUKEN49	911465	378	HMMER 1.8	PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop)	PF00063	53.97	125	274
			blastx.2	Myosin V.	sp AAF78910 AAF78910	66%	3	128
						54%	125	274
						40%	333	431
HCUDS02	914401	379	HMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	91.6	84	650
			blastx.2	CDNA FLJ10137 FIS, CLONE HEMBA1003136, WEAKLY SIMILAR TO 1	sp BAA91460 BAA91460	98%	78	782
						99%	907	1335
						64%	755	1006
HTTUJ40	914402	380	HMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	23.8	43	372
			blastx.2	GDP-MANNULOSE PYROPHOSPHORYLAS E A.	sp Q9Y5P5 Q9Y5P5	100%	40	417
						100%	440	496
HFXJX41	915649	381	HMMER 2.1.1	PFAM: Phosphoglucosyltransferase/phosphomannomutase	PF00408	36.5	491	682
			blastx.2	hypothetical protein b0644 - Escherichia coli	pir B64799 B64799	100%	3	308
						100%	308	496
						45%	6	308
						43%	3	308

HSLCK91	915650	382	HMMER 2.1.1	PFAM: Phosphoglucosyltransferase/phosphomannomutase	PF00408	36%	6	308
			blastx.2	phosphoglucosyltransferase (EC 5.4.2.2) - Escherichia coli	pir G64803 G64803	84%	1	375
			HMMER 2.1.1	PFAM: Serine hydroxymethyltransferase	PF00464	43	363	431
			blastx.2	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR 11	sp P34897 GLYM_H UMAN	92% 52% 48%	137 363 427	373 536 534
			HMMER 2.1.1	PFAM: Trypsin	PF00089	48.9	20	523
HRDBJ38	917583	384	blastx.2	SERINE PROTEASE (FRAGMENT).	sp O97658 O97658	62%	23	856
			HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	138.5	3	278
HOUES64	918119	385	blastx.2	lactaldehyde dehydrogenase (EC 1.2.1.22) aldA - Escherichia coli	pir A38165 A38165	98%	3	275
			HMMER 2.1.1					

HWLHU02	918520	386	HMMER 2.1.1 blastx.2	PFAM: Hexokinase Hexokinase II.	PF00349	286.7	3	395
HEAHA84	919363	387	HMMER 2.1.1 blastx.2	PFAM: Myosin head (motor domain) myosin I myr 4 - rat	sp CAA86476 CAA86476 PF00063	79% 66% 36.3	3 3 87	395 395 245
HBMXQ90	922114	388	HMMER 2.1.1 blastx.2	PFAM: Beta-ketoacyl synthase CDNA FLJ20604 FIS, CLONE KAT06449.	pir A53933 A53933 PF00109	96% 100% 20.5	87 794 218	794 1216 301
HOEJV72	930778	389	HMMER 1.8 blastx.2	PFAM: Nucleoside diphosphate kinases NM23-H7.	sp BAA91286 BAA91286 PF00334	66% 96% 103.55	301 215 362	462 301 757
HRDBH58	933364	390	HMMER 1.8 blastx.2	PFAM: Aldehyde dehydrogenases probable aldehyde dehydrogenase PA4073 [imported] - Pseudomonas aeruginosa (strain PAO1)	sp Q9Y5B8 Q9Y5B8 PF00171	95% 29% 175.49	89 368 536	847 754 1558
HCE3E13	951413	391	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (L, M and V) valine-tRNA ligase precursor, mitochondrial - fission yeast (Schizosaccharomyces pombe)	PF00133 pir T39630 T39630	95.6 40% 41% 44% 83%	148 151 4 569 645	603 603 213 649 662
HUKFO68	951652	392	HMMER	PFAM: Hexokinase	PF00349	173.1	83	340

			2.1.1	Hexokinase I (Fragment).	sp AAF28854 AAF28854	76%	83	355
			blastx.2			47%	83	373
						80%	3	80
						36%	3	77
HFXJW08	959204	393	HMMER 2.1.1	PFAM: tRNA synthetases class I (I, L, M and V)	PF00133	86.6	224	487
			blastx.2	leucine--tRNA ligase (EC 6.1.1.4) [validated] - Escherichia coli	pir H64798 SYECL	82%	224	676
						100%	3	230
HBTAD04	407351	394	blastx.2	malate synthase (EC 4.1.3.2) A - Escherichia coli	pir A32649 SYECMA	98%	240	1
HBTAD04	422687	868	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	36.5	427	161
HE8FG51	465267	395	HMMER 2.1.1	PFAM: Eukaryotic initiation factor 5A hypusine (eIF-5A)	PF01287	165.7	4	258
			blastx.2	EIF-5A2.	sp AAF98810 AAF98810	98%	7	267
HTPDU31	503077	396	HMMER 2.1.1	PFAM: haloacid dehalogenase-like hydrolase	PF00702	26.3	147	296
			blastx.2	DJ37E16.5 (NOVEL PROTEIN SIMILAR TO NITROPHENYLPHOSPHATASES 1	sp Q9UGY2 Q9UGY2	94%	54	323
						100%	25	72
						100%	323	364
HMUBV12	549423	397	HMMER 2.1.1	PFAM: Hyaluronidase	PF01630	50.7	196	303
HMHBS90	574062	398	HMMER	PFAM: UBA domain	PF00627	35.6	436	543

			2.1.1 blastx.2		HRHFB2157-LIKE PROTEIN (FRAGMENT).	sp Q9UHX4 Q9UHX 4	61% 100%	58 3	561 59
HLHGH34	575733	399	HMMER 1.8 blastx.2		PFAM: C-5 cytosine- specific DNA methylases PUTATIVE DNA CYTOSINE METHYLTRANSFERAS E DNMT2.	PF00145 sp O43669 O43669	33.72 100%	284 2	436 436
HELHC55	577384	400	HMMER 2.1.1 blastx.2		PFAM: Copper amine oxidase amine oxidase (copper- containing) (EC 1.4.3.6) tynA precursor - Escherichia coli	PF01179 pir E64889 E64889	88.8 96%	39 3	173 173
HKAAZ66	592105	401	HMMER 2.1.1 blastx.2		PFAM: Calpain family cysteine protease Calpain large polypeptide L2.	PF00648 sp AAF99682 AAF99 682	164.9 99% 98% 87%	222 90 416 648	422 422 640 671
HHSCN33	657367	402	HMMER 2.1.1 blastx.2		PFAM: HECT-domain (ubiquitin-transferase). NEDD4-like ubiquitin ligase 1.	PF00632 sp BAB13352 BAB1 3352	58.3 91%	166 1	348 390
HNGJQ15	660310	403	HMMER 2.1.1 blastx.2		PFAM: Histone deacetylase family CDNA FLJ10170 FIS, CLONE HEMBA1003690.	PF00850 sp BAA91474 BAA9 1474	33.2 75% 47%	70 70 196	192 192 264

HDJME16	661396	404	HMMER 2.1.1 blastx.2	WEAKLY SIMILAR TO 1 PFAM: FF domain	PF01846	53.7	34	183
HNTNR64	670033	405	HMMER 2.1.1 blastx.2	HUNTINGTON YEAST PARTNER C. PFAM: Kelch motif	sp Q9WVC9 Q9WV C9 PF01344	84%	1	486
HMICO24	677036	406	HMMER 2.1.1 blastx.2	CDNA FLJ11078 FIS, CLONE PLACE1005102, WEAKLY SIMILAR TO 1 PFAM: Kelch motif	sp BAA91990 BAA9 1990 PF01344	36% 34% 47% 43% 89.1	30 54 347 350 25	344 314 448 445 147
HSIAC23	679292	407	HMMER 2.1.1 blastx.2	LYMPHOCYTE ACTIVATION- ASSOCIATED PROTEIN. PFAM: Chlorohydrolase	sp Q9Y2X2 Q9Y2X2 PF01685	92% 49% 55% 44% 52% 80% 100% 100% 47%	25 25 55 25 85 285 242 2 236 194	261 243 231 243 234 344 283 22 286 358
HSLFL74	685897	408	HMMER 2.1.1	GUANINE DEAMINASE (EC 3.5.4.3) (GUANASE) (GUANINE 1) PFAM: RNB-like proteins	sp Q9R111 GUAD_ MOUSE PF00773	62% 87% 243.4	62 10 21	457 108 425

			blastx.2	exoribonuclease II (EC 3.1.13.1) - Escherichia coli	pir A64877 A64877	78%	705	1346
						97%	3	428
						75%	434	892
						94%	877	933
						48%	990	1064
HSDJD53	698259	409	HMMER 2.1.1	PFAM: Nitroreductase family	PF00881	86.9	193	513
			blastx.2	hypothetical protein, 20K (selD-sppA intergenic region) - Escherichia coli	pir A40360 A40360	80%	190	624
HCEBF33	702955	410	HMMER 2.1.1	PFAM: HECT-domain (ubiquitin-transferase).	PF00632	248.4	15	581
			blastx.2	Ubiquitin-protein ligase 1.	sp AAF36454 AAF36454	51%	21	581
HAPQW27	705518	411	HMMER 2.1.1	PFAM: Sterol O-acyltransferase	PF01800	180.1	1	279
			blastx.2	AGRP1 PROTEIN.	sp O75907 O75907	62%	1	432
HCFLZ28	707183	412	HMMER 2.1.1	PFAM: ThiF family	PF00899	93.7	166	444
			blastx.2	SUMO-1-ACTIVATING ENZYME E1 N SUBUNIT.	sp O95717 O95717	95%	142	447
						83%	495	545
HWCAB58	710377	413	HMMER 2.1.1	PFAM: Kelch motif	PF01344	53.3	21	164
			blastx.2	Kelch related protein 1.	sp CAC08185 CAC08185	49%	3	275
						59%	302	448
						29%	3	266
						28%	18	245
HLMMS57	713770	414	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	31	272	406

HMELH37	717556	415	blastx.2 HMMER 2.1.1	diamine N- acetyltransferase (EC 2.3.1.57) - spiny mouse (Mus saxicola)	pir S43430 S43430	39% 55%	272 55	478 135
			blastx.2	PFAM: Initiation factor 2 subunit family	PF01008	101.1	163	432
				probable translation initiation factor eIF-2B delta chain - human (fragment)	pir T08757 T08757	95% 96%	163 3	441 164
HNGJ55	722240	416	HMMER 2.1.1	PFAM: MaoC like domain	PF01575	117.2	16	285
			blastx.2	membrane protein maoC - Escherichia coli	pir F64889 F64889	100%	1	282
HNGJ55	868063	869	HMMER 2.1.1	PFAM: MaoC like domain	PF01575	117.2	308	577
HHGDG42	724795	417	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	24.9	179	313
			blastx.2	diamine N- acetyltransferase (EC 2.3.1.57) - spiny mouse (Mus saxicola)	pir S43430 S43430	40%	179	349
HMTMF31	731302	418	HMMER 2.1.1	PFAM: ThiF family	PF00899	88	50	415
			blastx.2	CG1749 PROTEIN.	sp Q9VYY3 Q9VYY 3	72%	62	424
HSDIF59	739212	419	HMMER 2.1.1	PFAM: Flavin reductase like domain	PF01613	139.4	411	683
			blastx.2	4- HYDROXYPHENYLAC	sp P75893 P75893	90%	294	740

HNDAG60	751953	420	HMME 2.1.1 blastx.2	ETATE 3- MONOOXYGENASE (EC 1.14.13.3). PFAM: Kelch motif	PF01344	53.8	177	320
				NS1-BINDING PROTEIN.	sp Q9Y480 Q9Y480	67% 75% 100% 36% 32% 34% 28% 30% 33%	174 296 3 174 174 174 323 174 320 418	425 445 80 323 320 320 436 320 418
HSLDS79	733247	421	HMME 2.1.1 blastx.2	PFAM: Trehalase alpha, alpha-trehalase (EC 3.2.1.28) precursor, periplasmic - Escherichia coli	PF01204	1028.4	117	1622
					pir S04782 S04782	100%	102	1622
HSLDS79	879215	870	HMME 2.1.1	PFAM: Trehalase	PF01204	102.4	132	392
HFBCQ61	769102	422	HMME 2.1.1 blastx.2	PFAM: Kelch motif hypothetical protein W02G9.2 - Caenorhabditis elegans	PF01344	83.8	117	245
					pir T33222 T33222	53% 41% 42% 37%	3 3 12 9	245 242 245 245
HRACD17	769103	423	HMME 2.1.1	PFAM: Kelch motif	PF01344	108.4	245	343

			blastx.2	CDNA FLJ10836 FIS, CLONE NT2RP4001228, WEAKLY SIMILAR TO 1	sp BAA91845 BAA9 1845	94%	2	358
HLDQV23	788957	424	HMMER 2.1.1	PFAM: Glycosyl transferases	PF00535	59.7	71	364
			blastx.2	hypothetical protein F13G3.6 - Caenorhabditis elegans	pir T20856 T20856	42%	68	376
HPHAF45	812327	425	HMMER 2.1.1	PFAM: Kelch motif	PF01344	88.4	22	162
			blastx.2	CDNA FLJ10262 FIS, CLONE HEMBB1000985, WEAKLY SIMILAR TO 1	sp BAA91514 BAA9 1514	100%	118	384
HSUME31	812373	426	HMMER 2.1.1	PFAM: Exonuclease	PF00929	118.4	4	441
			blastx.2	ISG20 PROTEIN.	sp O00441 O00441	57%	1	441
HUSHB56	815819	427	HMMER 2.1.1	PFAM: Calpain family cysteine protease	PF00648	70.1	101	346
			blastx.2	CALPAIN-LIKE PROTEASE.	sp Q9WVF0 Q9WVF 0	87%	65	352
HTGDN81	824708	428	HMMER 2.1.1	PFAM: RNB-like proteins	PF00773	395.6	417	1028
			blastx.2	virulence-associated protein vacB homolog - Escherichia coli	pir S56404 S56404	97% 94%	417 1	998 435

HSKHY26	836598	429	HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferases UDP- GALNAC:POLYPEPTID E.N- ACETYLGALACTOSA MINYLTRANSFERASE.	PF00535 sp Q9UIV5 Q9UIV5	66.5	35	427
HKACD80	837698	430	HMMER 2.1.1 blastx.2	PFAM: Glycosyl hydrolase family 47 CDNA FLJ10783 FIS, CLONE NT2RP4000417, WEAKLY SIMILAR TO 1	PF01532 sp BAA91806 BAA9 1806	125.1	198	521
HHFDK48	837782	431	HMMER 2.1.1 blastx.2	PFAM: Sulfatase N-acetylgalactosamine-4- sulfatase (EC 3.1.6.12) precursor - cat	PF00884 pir A44475 A44475	143.6	13	351
HE9SS77	838043	432	HMMER 2.1.1 blastx.2	PFAM: Sulfatase CG6725 PROTEIN.	PF00884 sp Q9VEX0 Q9VEX0	112.1	213	671
HAPOK49	848205	433	HMMER 2.1.1 blastx.2	PFAM: UBA domain BS4 PROTEIN (NY- REN-18 ANTIGEN).	PF00627 sp Q9Y5A7 BS4_HU MAN	61% 78.1	3 687	671 806
HPMGN48	848318	434	HMMER 2.1.1 blastx.2	PFAM: Initiation factor 2 subunit family CG11334 PROTEIN.	PF01008 sp Q9V9X4 Q9V9X4	77% 71% 89% 264.5	195 833 47 75	872 1063 187 572
						60%	78	605

HUVHP54	849278	435	HMMER 2.1.1 blastx.2	PFAM: Dienelactone hydrolase family Hypothetical 34.2 kDa protein.	PF01738 sp AAG12612 AAG1 2612	80.3 31%	354 330	1001 1001
HSLDK59	853385	436	HMMER 2.1.1 blastx.2	PFAM: N- acetylmuramoyl-L-alanine amidase hypothetical protein b0867 precursor - Escherichia coli	PF01510 pir C64825 C64825	80.6 100% 78%	500 500 183	736 1009 557
HMWDI41	854051	437	HMMER 2.1.1 blastx.2	PFAM: Kelch motif CDNA FLJ20059 FIS, CLONE COL01349.	PF01344 sp BAA90921 BAA9 0921	91.2 92%	488 2	595 592
HFVHU73	856165	438	HMMER 2.1.1 blastx.2	PFAM: RNB-like proteins ribonuclease II RNB family protein - fission yeast (Schizosaccharomyces pombe)	PF00773 pir T38518 T38518	62.5 45% 38%	6 9 253	281 281 360
HMUBJ80	858497	439	HMMER 2.1.1 blastx.2	PFAM: Histone deacetylase family CDNA FLJ10328 FIS, CLONE NT2RM2000588, WEAKLY SIMILAR TO 1	PF00850 sp BAA91545 BAA9 1545	44.9 93% 88%	233 209 477	430 490 602
HE9ML74	859297	440	HMMER 2.1.1 blastx.2	PFAM: HECT-domain (ubiquitin-transferase). CG5604 PROTEIN.	PF00632 sp Q9VL06 Q9VL06	74.3 82%	705 940	914 1269

HLQAJ01	864092	441	HMMER 2.1.1 blastx.2	PFAM: Histone deacetylase family Class I histone deacetylase.	PF00850 sp AAF73076 AAF73 076	40% 43% 24.3	456 3 13	932 350 90
HSLDP32	866241	442	HMMER 2.1.1 blastx.2	PFAM: Fumarylacetoacetate (FAA) hydrolase family conserved hypothetical protein PA0318 [imported] - Pseudomonas aeruginosa (strain PAO1)	PF01557 pir G83604 G83604	100% 39.8	7 78	240 197
HPMEG40	866272	443	HMMER 2.1.1 blastx.2	PFAM: Asparagine synthase asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Escherichia coli	PF00733 pir A36616 AJECN	244.9 72% 98% 87%	270 270 31 589	590 656 267 636
HRADE27	867195	444	HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferases group 1 L165.1 (Fragment).	PF00534 sp AAF77213 AAF77 213	25 40% 44%	125 50 385	403 409 531
HTXQR10	869137	445	HMMER 2.1.1 blastx.2	PFAM: Kelch motif KELCH MOTIF CONTAINING PROTEIN.	PF01344 sp Q9Y2M5 Q9Y2M 5	94.1 44% 32% 43% 34% 36%	283 166 166 181 166 181	423 381 531 366 381 363